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(54) **METHODS OF USING FIELD-DERIVED COLONIES OF INSECTS SELECTED FOR DECREASED SUSCEPTIBILITY TO PLANTS EXPRESSING INSECTICIDAL TOXINS**

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CPC . A01K 67/033; A01N 20/00; C12N 15/8286; G01N 33/5085
See application file for complete search history.

(56) **References Cited**

FOREIGN PATENT DOCUMENTS

WO WO 2009/132850 * 11/2009 C12N 15/82

OTHER PUBLICATIONS

M. Willrich Siebert et al., Efficacy of CRY1F Insecticidal Protein in Maize and Cotton for Control of Fall Armyworm (Lepidoptera: Noctuidae). Florida Entomol, 2008, 91:555-565.*

Adamczyk et al., Larval Survival and Development of the Fall Armyworm (Lepidoptera: Noctuidae) on Normal and Transgenic Cotton Expressing the Bacillus thuringiensis Cry1A (c) a-endotoxin. Journal of Economic Entomology. 1998, vol. 91, No. 2: 539-545.*
Farias et al., Field-evolved resistance to Cry1F maize by Spodoptera frugiperda (Lepidoptera: Noctuidae) in Brazil. Crop Protection 64 (2014) 150-158.*

Storer, et al., "Discovery and Characterization of Field Resistance to Bt Maize: Spodoptera frugiperda (Lepidoptera: Noctuidae) in Puerto Rico", Journal of Economic Entomology; vol. 103(4):1031-1038 (2010).

Liu, et al., "Resistance Allele Frequency to Bt Cotton in Field Populations of Helicoverpa armigera (Lepidoptera: Noctuidae) in China", Journal of Economic Entomology; vol. 101(3): 933-943 (2008).

Gould, et al., "Initial frequency of alleles for resistance to Bacillus thuringiensis toxins in field populations of Heliothis virescens", Proceedings of the National Academy of Sciences; vol. 94(8): 3519-3523 (1997).

Liu, et al., "Evidence of field-evolved resistance to Cry1Ac-expressing Bt cotton in Helicoverpa armigera (Lepidoptera: Noctuidae) in northern China", Pest Management Science; vol. 66(2): 155-161 (2009).

Xu, et al., "Using an F 2 screen to monitor frequency of resistance alleles to Bt cotton in field populations of Helicoverpa armigera (Hubner) (Lepidoptera: Noctuidae)", Pest Management Science; vol. 65(4): 391-397 (2009).

Adamczyk, J.J., et al., "Increased Tolerance of Fall Armyworms (Lepidoptera: Noctuidae) to Cry1Ac d-Endotoxin when Fed Transgenic Bacillus thuringiensis Cotton: Impact on the Development of Subsequent Generations", Florida Entomologist; vol. 84(1): 1-6; 2001.

Hernandez, C., et al., "Common Receptor for Bacillus thuringiensis Toxins Cry1Ac, Cry1Fa, and Cry1Ja in Helicoverpa armigera, Helicoverpa zea, and Spodoptera exigua", Applied and Environmental Microbiology; vol. 71(9): 5627-5629; 2005.

Siebert, M., et al., "Evaluation of Corn Hybrids Expressing Cry1F (Herculex I Insect Protection) Against Fall Armyworm (Lepidoptera: Noctuidae) in the Southern United States", J. Entomol. Sci.; vol. 43(1) 41-51; 2008.

* cited by examiner

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(57) **ABSTRACT**

Methods are provided for using field-derived colonies of insects that comprise field-evolved resistance to insecticidal toxins that are produced in transgenic plants. The methods find use in resistance management strategies for transgenic crop plants expressing insecticidal toxins.

6 Claims, 2 Drawing Sheets

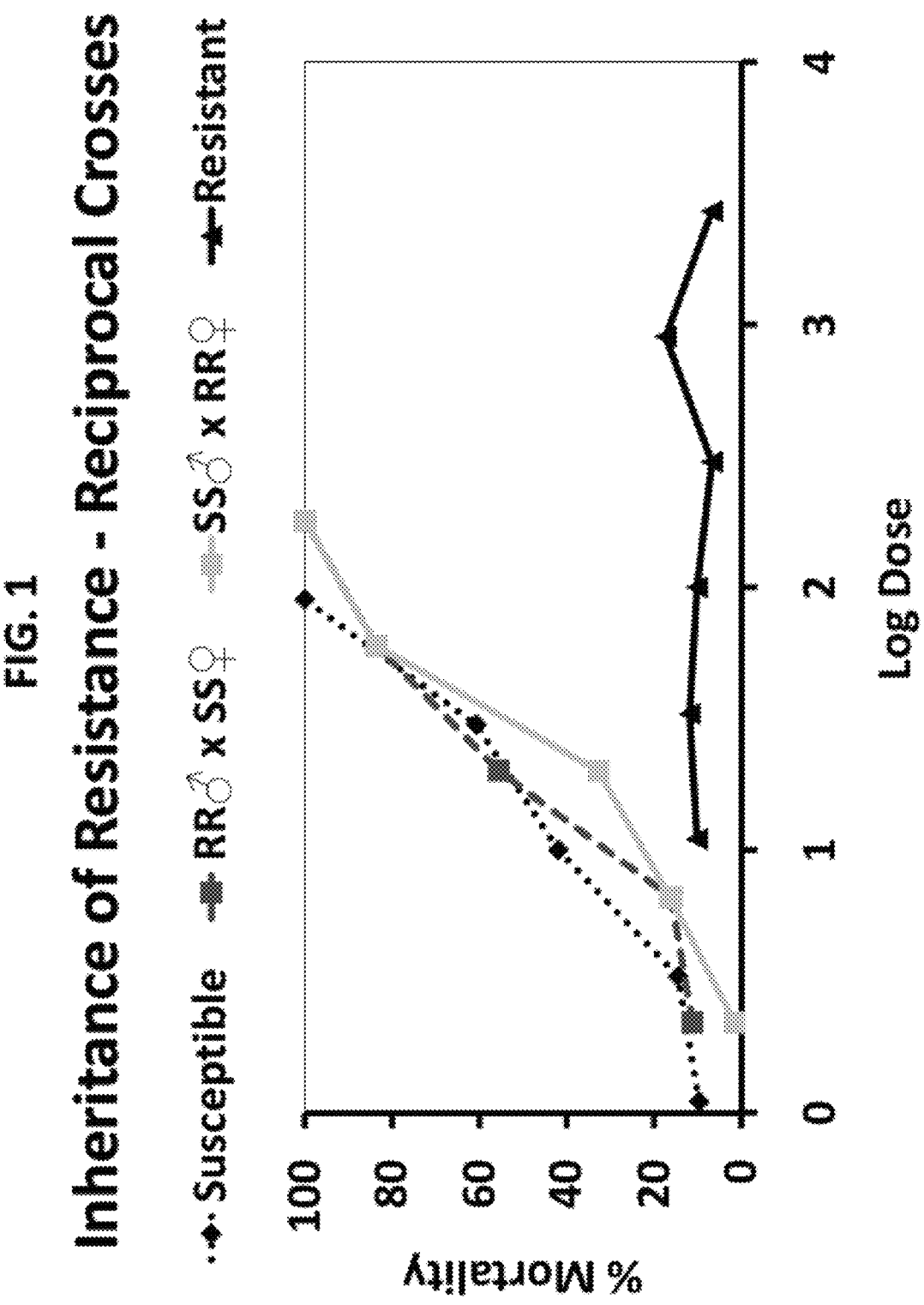
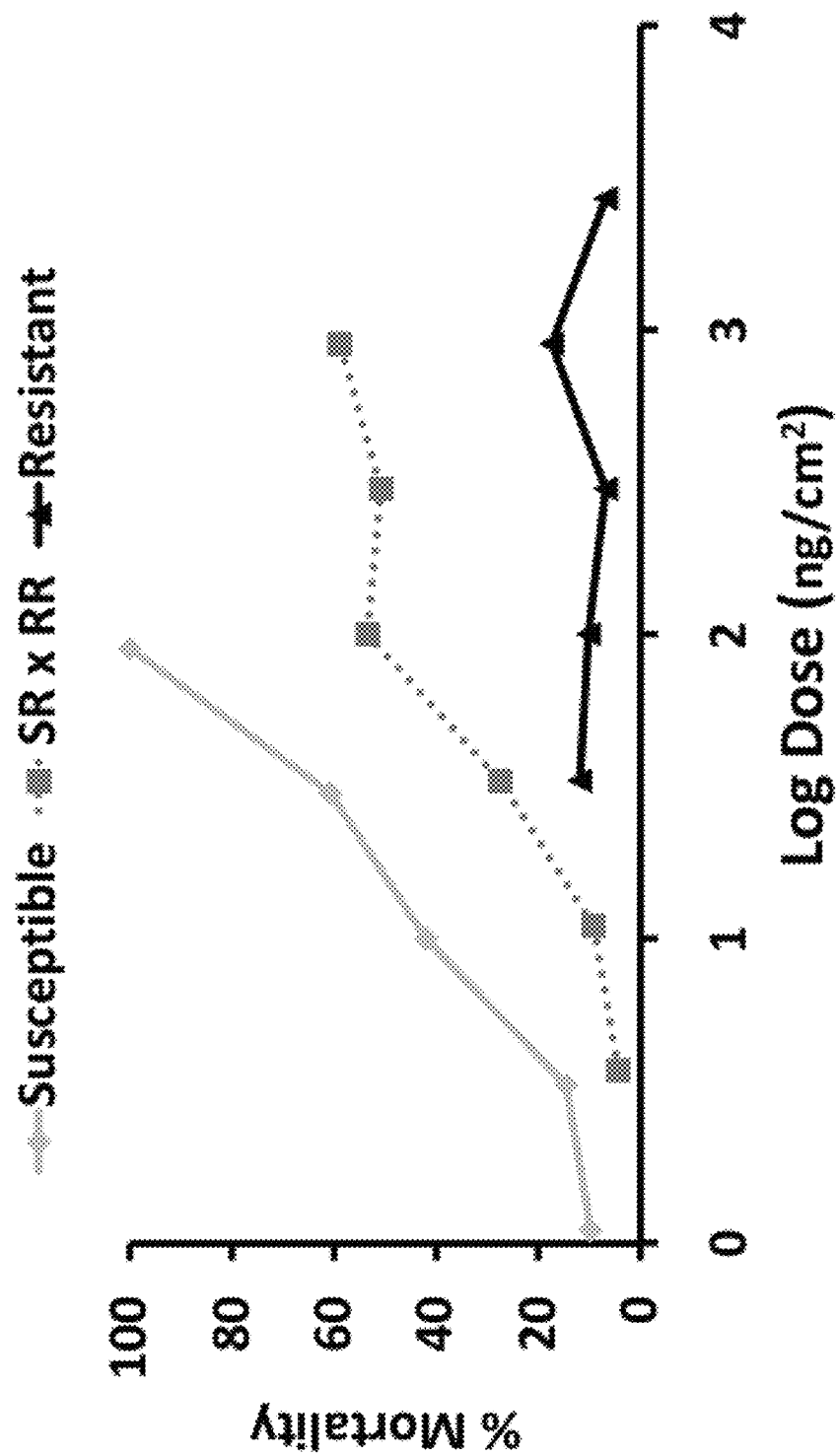


FIG. 2
Inheritance of Resistance - Backcrosses



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METHODS OF USING FIELD-DERIVED COLONIES OF INSECTS SELECTED FOR DECREASED SUSCEPTIBILITY TO PLANTS EXPRESSING INSECTICIDAL TOXINS

CROSS REFERENCE TO RELATED APPLICATIONS

This application claims priority under 35 U.S.C. §119(e) to provisional application Ser. No. 61/422,216 filed Dec. 12, 2010, herein incorporated by reference in its entirety.

FIELD OF THE INVENTION

The present invention relates to methods of using field-derived colonies of insects with increased tolerance to transgenic crop plants expressing insecticidal toxins.

BACKGROUND OF THE INVENTION

Corn, *Zea mays* L., is one of the crops most widely grown in the United States, with over 60 million acres of corn planted annually (Andow and Hutchison (1998) "Bt-corn resistance management". In *Now or never: serious new plans to save a natural pest control*, eds. Mellon and Rissler, eds., pp. 19-66, Union of Concerned Scientists, Cambridge, Mass.). Fall armyworm (FAW, *Spodoptera frugiperda* (J. E. Smith)) is one of the most important lepidopteran pests of corn in southern United States (Buntin (2008) *Florida Entomol.* 91:523-530), as well as Latin and South Americas. Damage by FAW involve leaf feeding, often observed in whorl stage plants, as well as ear feeding, causing substantial yield losses. Insecticidal control to prevent ear damage in field corn is difficult and generally not cost effective. Transgenic corn expressing *Bacillus thuringiensis* (Bt) insecticidal toxins is an effective control technology against FAW offering great potential for reducing losses by this insect pest in field corn (Buntin et al. (2001) *Florida Entomol.* 84:37-42; Buntin et al. (2004) *J. Econ. Entomol.* 97:1603-1611). However, there is a concern that insects may rapidly develop resistance to the Bt expressed in plants in areas where continuous use and intensive selection pressure is applied (Mallet and Porter (1992) *Proc. R. Soc. B* 250:165-169; Chaufaux et al. (2001) *J. Econ. Entomol.* 94:1564-1570).

Insect resistance evolution has been well documented and is a serious problem in agricultural and livestock production, urban environments, and public health (Georghiou (1986) "The magnitude of resistance problem," In *Pesticide Resistance: strategies and tactics for management*, Council, ed., pp. 14-44, National Academy Press, Washington, D.C.; Roush and McKenzie (1987) *Annu. Rev. Entomol.* 32:361-380, Roush and Tabashnik (1990) *Pesticide resistance in arthropods*, New York, N.Y., Chapman and Hall). Bt is a valuable source of insecticidal proteins for use in insect pest control either in conventional spray formulations or in transgenic crops (Roush (1994) *Biocontrol Sci. Technol.* 4:501-516; Ferré and J. Van Rie (2002) *Annu. Rev. Entomol.* 47:501-533). Nonetheless, the evolution of insect resistance in field populations is an important threat to this technology (Ferré and J. Van Rie (2002) *Annu. Rev. Entomol.* 47:501-533), especially with transgenic plants that express Bt toxins (Mallet and Porter (1992) *Proc. R. Soc. B* 250:165-169).

Maize hybrids containing event TC1507 express both Cry1F and PAT genes. The Cry1F protein confers resistance to key Lepidopteran pests of maize, such as European corn borer (*Ostrinia nubilalis*), southwestern corn borer (*Diatraea grandiosella*), FAW, and black cutworm (*Agrotis ipsilon*).

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The pat gene encodes the PAT protein to confer tolerance to the herbicidal active ingredient glufosinate-ammonium. Maize hybrids containing event TC1507 have been widely adopted in the United States since its commercialization in 1998. As part of the regulatory submission a mandated insect resistance management (IRM) plan was proposed to delay the rate of evolution of resistance. Currently, the preferred and most widely adopted strategy involves the use of plants expressing a high dose of the Bt toxin in conjunction with planting a refuge of a non-Bt crop for preservation of susceptible genes (International Life Sciences Institute. Health and Environmental Sciences Institute (1999) *An evaluation of insect resistance management in Bt field corn: A science-based framework for risk assessment and risk management*; Tabashnik et al. 2003. *J. Econ. Entomol.* 96:1031-1038). This approach was considered to be most feasible and realistic in terms of farming practices and in prolonging the use of Bt transgenic crops (Gould (1998) *Annu. Rev. Entomol.* 43:701-726). However, there still is a concern that insects may develop resistance to the Bt expressed in plants in areas where continuous use and intensive selection pressure is applied (Mallet and Porter (1992) *Proc. R. Soc. B* 250:165-169; Chaufaux et al. (2001) *J. Econ. Entomol.* 94:1564-1570).

FAW populations in Puerto Rico have been exposed to microbial Bt formulation used in conventional insecticides, and to transgenic plants containing event TC1507 over several years, both containing Bt Cry1 insecticidal proteins. Even though the Cry1F toxin is uniquely efficacious in controlling FAW when compared to other Cry1 toxins (Waquil et al. (2002) *Revista Brasileira de Milho e Sorgo* 1:1-11; Waquil et al. (2004) *Revista Brasileira de Milho e Sorgo* 3:161-171), repeated exposures to this toxin and the unique conditions of Puerto Rico (i.e., tropical island geography, reduced availability of alternative hosts due to drought conditions, continuous corn growth, and high population density with overlapping generations) collaborated for increased pest population selection pressure and therefore increased likelihood for evolution of resistance.

BRIEF SUMMARY OF THE INVENTION

The present invention discloses the production of a field-derived colony of fall armyworm (FAW, *Spodoptera frugiperda*) selected for decreased susceptibility to maize plants expressing the insecticidal protein Cry1F. Thus, in one aspect the invention provides methods for producing a field-derived colony of FAW that comprises decreased susceptibility to maize plants producing Cry1F. FAW from such a field-derived colony comprise field-evolved resistance to Cry1F. The methods involve collecting FAW from a field comprising maize plants, particularly a field comprising maize plants that produce Cry1F, feeding the FAW leaf material from maize plants that express Cry1F, and selecting FAW individuals that survived exposure. The methods can further involve transfer of the surviving FAW to a standard fall armyworm diet that lacks Cry1F to allow the survivors to complete development. The methods can further involve allowing the surviving FAW to mate to maintain the colony with selection periodically applied in subsequent generations by feeding the FAW leaf material from maize plants that express Cry1F and selecting surviving FAW, and therefore fixing resistance by eliminating individuals that do not carry homozygous resistance alleles. It is recognized that the methods for producing a field-derived colony of FAW can be used in a like manner with other any other insect pest of that evolves resistance to one or more insecticidal toxins, particular one or more *Bacillus thuring-*

iensis (Bt) insecticidal toxins, that produced a transgenic plant, particularly a transgenic crop plant.

In one embodiment, the methods of the present invention were used to produce a field-derived colony of FAW (referred to herein as "FAW-SPR") with fixed alleles for resistance from eggs collected in Puerto Rico, USA in a field of transgenic maize plants comprising maize event TC1507, which express Cry1F. The FAW from this colony display decreased susceptibility to maize plants comprising maize event TC1507.

The present invention further provides methods for determining the frequency of resistance alleles in populations where resistance has not evolved. The methods involve collecting insects from a field or other site, mating virgin adults from the collected insects with virgin adult insects from a field-derived colony of the resistant insect of the same species as the collected insects, allowing larvae from the mating to feed on a diet comprising an insecticidal toxin at a concentration that is lethal to susceptible insects, and determining mortality. Such methods find use, for example, in the development of resistance management strategies.

In one embodiment of the invention, methods for determining the frequency of resistance alleles in populations of FAW where resistance to Cry1F has not evolved. The methods involve collecting FAW from a field or other site, mating virgin adults from the collected FAW with virgin adults from resistant FAW from the field-derived colony, allowing larvae from the mating to feed on a diet comprising Cry1F at a concentration that is lethal to susceptible FAW, and determining mortality. Such methods find use, for example, in the development of resistance management strategies.

The present invention further provides methods of using a field-derived colony of an insect pest of interest that comprises an insect pest of interest with field-evolved resistance to an insecticidal toxin that is expressed in a transgenic plant. Such a field-derived colony of an insect pest of interest can be produced, for example, by the methods disclosed herein or by any other method known in the art. The methods of the invention include, for example, using such a field-derived colony of an insect pest of interest in methods: for understanding the mechanism of the insect resistance to insecticidal toxin; for evaluating cross-resistance potential of the insecticidal toxin with any other existing or new insecticides or insecticidal proteins with activity against the insect pest of interest; to improve resistance monitoring strategies for the insect pest of interest in geographic locations where crop plants expressing the insecticidal toxin have been commercialized or are planned to be commercialized; of validating assumptions used in known resistance-risk computer simulation models for crop plants expressing the insecticidal toxin; for evaluating alternative refuge deployment strategies for crop plants, such as, for example, seed mixes or refuge-in-a-bag strategies; of investigating whether or not existing insect control tactics will affect the rate at which the insect pest of interest may develop resistance to transgenic crop plants expressing the insecticidal toxin under field conditions; to develop molecular marker technology to monitor for the development of resistance (change in resistant alleles' frequency) to the insecticidal toxin in field populations of the insect pest of interest; and to provide a better understanding on the mode of action of the insecticidal toxin in the control of the insect pest of interest.

In one embodiment of the invention, the insect pest is FAW and the insecticidal toxin is Cry1F expressed in transgenic maize plants, particularly transgenic maize plants comprising maize event TC1507. The methods of the invention include, for example, using such a field-derived colony of FAW in

methods: for understanding the mechanism of fall armyworm resistance to Cry1F; for evaluating cross-resistance potential of Cry1F with any other existing or new insecticides or insecticidal proteins with activity against fall armyworm; to improve fall armyworm resistance monitoring strategies for TC1507 in maize in the continental U.S.A. and other geographic locations where event TC1507 maize has been commercialized or is planned to be commercialized; of validating assumptions used in known resistance-risk computer simulation models for maize event TC1507; for evaluating alternative refuge deployment strategies for event TC1507 maize, such as, for example, seed mixes or refuge-in-a-bag strategies; of investigating whether or not existing fall armyworm control tactics, namely MON810 and Bt11 maize plants, both of which express Cry1Ab, and chemical insecticides, will affect the rate at which fall armyworm may develop resistance to TC1507 under natural field conditions; to develop molecular marker technology to monitor for the development of resistance (change in resistant alleles' frequency) to Cry1F in field populations of FAW; and to provide a better understanding on the mode of action of the Cry1F toxin in the control of FAW.

BRIEF DESCRIPTION OF THE FIGURES

FIG. 1 is a mortality curve from reciprocal crosses of FAW from FAW-SPR to susceptible FAW as described in Example 5.

FIG. 2 is a mortality curve from Sr, rr FAW and backcrosses of rS to a FAW as described in Example 5.

DETAILED DESCRIPTION OF THE INVENTION

The present invention now will be described more fully hereinafter with reference to the accompanying drawings, in which some, but not all embodiments of the inventions are shown. Indeed, these inventions may be embodied in many different forms and should not be construed as limited to the embodiments set forth herein; rather, these embodiments are provided so that this disclosure will satisfy applicable legal requirements. Like numbers refer to like elements throughout.

Insect colonies resistant to toxins in general provide a great means to evaluate risks associated with resistance evolution, validate resistance management strategies, and improve resistance management practices. Furthermore, they serve as powerful tool for elucidating several aspects related to insecticide resistance, including the mode of action of insecticides, predicting or determining the mechanism of insect resistance, understanding the genetics associated with insect resistance, and for the discovery or design of new insect control tactics that will minimize the possibility of cross-resistant to existing control technologies. Traditional methods of creating insect resistance to a control tactic involve exposure of laboratory-adapted susceptible strains (or field collected susceptible insect populations) to increasing concentrations of the toxin on artificial diet, and maintaining any survivors after every generation of exposure. Disadvantages associated with this technique include the large number of individuals required to generate the colony, especially if the frequency of resistance alleles are extremely rare in the population. Moreover, because the selection pressure applied to laboratory-selected colonies is generally lower than what is observed in the field, often times this type of regime selects for individuals that do not necessarily reproduce mechanisms of resistance that will likely develop under field conditions.

The availability of insect colonies with developed resistance to chemical insecticides, or plant-incorporated protectants, in case of transgenic plants expressing insecticidal toxins, aids in understanding the relative importance of any changes in susceptibility detected in field populations through routine monitoring. Furthermore, it provides researchers with the opportunity to improve the sensitivity of monitoring techniques by identifying the gene or genes responsible for resistance (e.g. use of high-throughput molecular tools to detect the presence of resistant genes in field populations from different geographies, and monitor changes in allele frequency). Additionally, information generated from such colonies are particularly valuable as input parameters in modeling attempts.

The availability of a field-derived selected FAW colony that survives exposure to leaf material expressing Cry1F toxin is especially useful in evaluating such risks, as well as validating and improving resistance management. Because the FAW-SPR was selected for Cry1F resistance in the field, information generated from this colony will especially be field relevant and will improve our ability to mitigate resistance development to preserve the durability of TC1507 in geographic areas where resistance alleles are still found in lower frequency.

The present invention discloses the production of a fall armyworm colony from several hundred egg collected in corn fields in Puerto Rico in October 2008 and January 2009. Because of the origin of the eggs in Puerto Rico, the colony has been named the "Selected Puerto Rico Colony" which is referred to here as "FAW-SPR". FAW from this colony comprises field-evolved resistant to Cry1F.

As used herein, "field-evolved resistance to Cry1F" means a heritable trait of FAW that confers on the FAW enhanced tolerance to the insecticidal effects of Cry1F and that originated from an agricultural field or other non-laboratory environment. An FAW that displays the field-evolved resistance to Cry1F will be able to survive on diet comprising a higher concentration of Cry1F than a susceptible FAW that does not express the resistance trait. In one embodiment of the invention, the field-evolved resistance to Cry1F FAW will be due to a single gene or genetic locus, and in other embodiments, two or more genes can be involved. Moreover, it is recognized that the field-evolved resistance can be dominant, semi-dominant, or recessive. In one embodiment of the invention, a field-derived colony of FAW comprising field-evolved resistance to Cry1F was produced by methods of the present and invention and the field-evolved resistance to Cry1F was determined to be due to a single gene or genetic locus and the resistance was recessive. Thus, only FAW that are homozygous for the resistance allele display enhanced resistance to Cry1F, when compared to similar FAW that lack two copies of the resistance allele.

As used herein, "susceptible FAW", or "susceptible fall armyworm" or "susceptible individuals" means a fall armyworm (or army worms) that do not display that enhanced tolerance to Cry1F as disclosed herein.

The present invention relates to the production of a fall armyworm colony comprising field-evolved resistance to the insecticidal protein Cry1F. Because the resistance to Cry1F evolved in an agricultural field, it is believed that the use of such FAW in methods, for example, for developing resistance management strategies, is more advantageous than the use of resistant FAW that was produced via a laboratory-based, artificial-selection procedure. Thus, the field-derived FAW colonies of the present invention find use a number of improved

methods related to, for example, resistance management and understanding the mechanism of fall armyworm resistance to Cry1F.

The present invention discloses the production of a field-derived colony of fall armyworm (FAW, *Spodoptera frugiperda*) selected for decreased susceptibility to maize plants expressing the insecticidal protein Cry1F. Thus, in one aspect the invention provides methods for producing a field-derived colony of FAW that comprises decreased susceptibility to maize plants producing Cry1F. FAW from such a field-derived colony comprise field-evolved resistance to Cry1F.

The methods for producing a field-derived colony of FAW that comprises decreased susceptibility to maize plants producing Cry1F involve collecting FAW, preferably FAW comprising resistance to Cry1F, from a field, particularly an agricultural field comprising one or more maize plants, more particularly an agricultural field comprising one or more maize plants that express the insecticidal protein Cry1F, most particularly an agricultural field comprising one or more maize plants comprising event TC1507. Maize plants comprising event TC1507 are transgenic maize plants that produce in their leaves Cry1F from a transgene comprising a maize ubiquitin (Ubi-1) gene promoter operably linked to a DNA molecule encoding a *Bacillus* delta-endotoxin identified as Cry1F. Maize plants comprising event TC1507 have been previously disclosed. See, U.S. Pat. Nos. 7,449,564; 7,435,807; 7,417,132; and 7,288,643; all of which are hereby incorporated in their entirety by reference. Cry1F has also been previously disclosed. See, U.S. Pat. Nos. 5,188,960 and 6,218,188; both of which are hereby incorporated in their entirety by reference.

Typically, the FAW will be collected from one or more agricultural fields in which the evolution of resistant FAW is suspected because of the observation of increased numbers of FAW in such agricultural fields which is indicative of the evolution of resistance in a population of maize plants previously comprised only susceptible FAW.

The FAW can be collected at any life stage (e.g., egg, larvae, pupa, and adult) although it is preferable to collect eggs as a matter of convenience. If eggs are collected, they can be hatched and resulting larva (neonates) allowed to feed on a diet comprising Cry1F at an effective concentration that is sufficient to kill all susceptible FAW but not FAW with field-evolved resistance. In a preferred embodiment of the invention, the larvae are fed leaf material from maize plants that express Cry1F, particularly maize plants comprising maize event TC1507.

It is recognized that an effective concentration of Cry1F can be determined by methods known in the art involving varying the concentration of Cry1F fed to both susceptible and resistant individuals and counting survivors after a certain period of exposure. It is recognized that methods can be also be used to determine LC_{50} , which is the lethal concentration at which 50% of individuals exposed to Cry1F do not survive.

The larvae (neonates) are allowed to feed on the Cry1F-containing diet for a period time sufficient to kill susceptible larvae and the surviving FAW selected. Generally, the period of time the larvae are exposed to the Cry1F-containing diet is at least 1, 2, 3, 4, 5, 6, 7, or more days, preferably between 2 and 6 days, more preferably between 3 and 5 days, most preferably 4 days.

The methods of the invention can further involve transfer of the surviving FAW to a standard fall armyworm diet that lacks Cry1F to allow the survivors to complete development. Such a diet can, for example, comprise maize leaf material that does not comprise Cry1F.

The methods can further involve allowing the surviving FAW to mate to maintain the colony with a secondary selection periodically applied in subsequent generations by feeding the FAW a diet as described above that comprises Cry1F at an effective concentration that is sufficient to kill all susceptible FAW but not FAW with field-evolved resistance from maize plants that express Cry1F. The methods can further involve selecting surviving FAW.

Typically, this secondary selection to maintain the field-evolved resistance in the colony will be applied every third generation although the invention does not depend on applying a secondary selection at a particular generation. The secondary selection only need be applied frequently enough to maintain to field-evolved resistance in the colony. Thus, the secondary selection can be applied to each generation, to the second generation, the third generation, the fourth generation, the fifth generation, or an even later generation.

In one embodiment, the methods of the present invention were used to produce a field-derived colony of FAW, referred to herein as "FAW-SPR", from eggs collected in Puerto Rico, USA in a field of transgenic maize plants comprising maize event TC1507. The FAW from this colony display decreased susceptibility to maize plants comprising maize event TC1507. The FAW-SPR colony was produced essentially as follows.

1. The Selected Puerto Rico Colony of fall armyworm (FAW-SPR) was initiated by collecting at least 1000 fall armyworm eggs from fields comprising maize plants comprising maize event TC1507 in Puerto Rico in October 2008 and January 2009.
2. Upon arrival at the laboratory, the eggs were incubated at approximate 25° C. until hatching. Hatching occurred within 1 day.
3. The recently hatched larvae (neonates) were exposed to Cry1F expressing leaf disks and allowed to grow for 4 days.
4. Survivors were collected and transferred to a standard fall armyworm diet lacking Cry1F (e.g., isoline corn) and allowed to complete development.
5. Individuals completing development are allowed to mate in order to maintain the colony.
6. Every three generations, selection in Cry1F expressing leaf tissue is conducted using a population of at least 500 neonates.

The present invention further provides methods for determining the inheritance of resistance of in a field-derived colony of FAW that comprises field-evolved resistance to Cry1F. The methods involve mating resistant FAW from the field-derived colony with FAW that are susceptible to Cry1F, preferably in reciprocal crosses, and analyzing the mortality rates of the progeny from each mating when grown in the presence of Cry1F. The methods can also involve backcrossing the progeny from each mating to resistant FAW. Such methods can be used to determine if the resistance to Cry1F is dominant, semi-dominant, or recessive or if sex-linkage is involved and can also be used to determine the number of resistance genes.

The present invention further provides methods for determining the frequency of resistance alleles in a population in which resistance has not evolved. The methods involve collecting insects of a insect pest of interest from a field or other non-laboratory site, mating virgin adults from the collected insects with virgin adults from resistant insects from a field-derived colony of the insect pest of interest whereby progeny larvae are produced and wherein the resistant insects comprise resistance to an insecticidal toxin, allowing the progeny larvae from the mating to feed on a diet comprising the

insecticidal toxin at a concentration that is lethal to susceptible insects of insect pest of interest but not lethal to resistant insects of insect pest of interest, and determining mortality. Such methods find use, for example, in the development of resistance management strategies.

In one embodiment of the present invention, the methods for determining the frequency of resistance alleles in a population in which resistance has not evolved comprise collecting FAW from a field or other non-laboratory site, mating virgin adults from the collected FAW with virgin adults from the resistant FAW from the field-derived colony, allowing larvae from the mating to feed on a diet comprising Cry1F at a concentration that is lethal to susceptible FAW but not lethal to resistant FAW, and determining mortality. Such methods find use, for example, in the development of resistance management strategies.

The present invention further provides methods of using a field-derived colony of an insect pest of interest that comprises an insect pest of interest with field-evolved resistance to an insecticidal toxin that is expressed in a transgenic plant, particular a transgenic crop plant. Such a field-derived colony of an insect pest of interest can be produced, for example, by the methods disclosed herein or by any other method known in the art. Such field-derived colonies include, for example, those disclosed in Tabashnik et al. ((2009) *J. Econ. Entomol.* 102:2011-2025).

The methods of the invention include, for example, using such a field-derived colony of an insect pest of interest in methods: for understanding the mechanism of the insect resistance to insecticidal toxin; for evaluating cross-resistance potential of the insecticidal toxin with any other existing or new insecticides or insecticidal proteins with activity against the insect pest of interest; to improve resistance monitoring strategies for the insect pest of interest in geographic locations where crop plants expressing the insecticidal toxin have been commercialized or are planned to be commercialized; of validating assumptions used in known resistance-risk computer simulation models for crop plants expressing the insecticidal toxin; for evaluating alternative refuge deployment strategies for crop plants, such as, for example, seed mixes or refuge-in-a-bag strategies; of investigating whether or not existing insect control tactics will affect the rate at which the insect pest of interest may develop resistance to transgenic crop plants expressing the insecticidal toxin under field conditions; to develop molecular marker technology to monitor for the development of resistance (change in resistant alleles' frequency) to the insecticidal toxin in field populations of the insect pest of interest; and to provide a better understanding on the mode of action of the insecticidal toxin in the control of the insect pest of interest.

The present invention further provides methods of using a field-derived colony of FAW that comprises FAW with field-evolved resistance to Cry1F. Such a field-derived colony of FAW can be produced, for example, by the methods disclosed herein or by any other method known in the art. In general such methods relate to the management of resistance to FAW in maize plants comprising Cry1F and to understanding the mechanism of fall armyworm resistance to Cry1F. A number of such methods of using a field-derived colony of FAW that comprises FAW with field-evolved resistance to Cry1F are disclosed below, although many modifications and other embodiments of the methods set forth herein will come to mind to one skilled in the art to which these inventions pertain having the benefit of the teachings presented in the foregoing descriptions and the associated drawings.

The methods of the invention include, but are not limited to, using a field-derived colony of FAW that comprises FAW with field-evolved resistance to Cry1F:

1. To understand the mechanism of fall armyworm resistance to Cry1F. This information will assist in the design and development of novel tactics for fall armyworm resistance management. The most frequent mechanism of *B. thuringiensis* toxins resistance is binding site modification, which has been shown to be the basis of cross-resistance among Cry1A toxins (Ferré and J. Van Rie (2002) *Annu. Rev. Entomol.* 47:501-533). From a resistance management perspective, toxins that act on the same binding sites should not be used as complements or replacements for each other. For example, several insect species have shown common binding sites for Cry1A and Cry1Ja, apparently a general pattern in lepidopteran species (Hua et al. (2001) *App. Environ. Microbiol.* 67:872-879). Hernandes and Ferré ((2005) *Appl. Environ. Entomol.* 71:5627-5629) have shown that *Helicoverpa armigera*, *Helicoverpa zea*, and *Spodoptera exigua* share a common receptor for Cry1Ac, Cry1Fa, and Cry1Ja through binding studies using ¹²⁵I-Cry1Ac and biotinylated Cry1Fa toxins. This study was conducted using susceptible laboratory strains. The availability of a field derived FAW resistance strain will allow, for example, for the generation of field-relevant information that may assist in the development of resistance management strategies.
2. To evaluate cross-resistance potential of Cry1F with any other existing or new insecticides or insecticidal proteins with activity against fall armyworm. This information will assist in the development of new product concepts as single traits or in combination with TC1507 to minimize the likelihood of resistance development in areas where resistance has not evolved. Cross-resistance studies with new actives are commonly conducted using diet-based bioassays as described by Pereira et al ((2008) *Entomologia Experimentalis et Applicata* 126: 115-121) and Siqueira et al. ((2004) *J. Pest Manag. Sci.* 90:1189-1196).
3. To evaluate cross-resistance potential of TC1507 with any current fall armyworm actives that may be used in combination to TC1507 to minimize the likelihood of resistance development in areas where resistance has not evolved. Cross-resistance studies with commercially available actives are commonly conducted using diet-based bioassays or tissue-based bioassays as described by Pereira et al ((2008) *Entomologia Experimentalis et Applicata* 126:115-121), Siqueira et al. ((2004) *J. Pest Manag. Sci.* 90:1189-1196, and Crespo et al. ((2009) *Pest Manag. Sci.* 65:1071-1081).
4. To improve fall armyworm resistance monitoring strategies for TC1507 in maize in the continental U.S.A. and other geographic locations where event TC1507 is or will be commercialized, FAW is a major pest and resistance has not evolved. This can be done by estimating frequency of resistance alleles in populations where resistance has not evolved using either an F1 or F2 screen, as described by Gould et al. ((1997) *PNAS* 94:3519-3523) and Andow and Alstad ((1998) *J. Econ. Entomol.* 91:572-578), respectively.
5. To validate assumptions used in the resistance-risk computer simulation model for event TC1507. For example, computer simulations based on empirically derived parameters, such as mortality and dispersal estimates, would serve as an improved tool to better indicate whether different refuge deployment strategies would

- have an impact in delaying the evolution of resistance in different insect population species (Davis and Onstad 2000). Empirically derived parameters obtained from both susceptible and resistance strains will strengthen predictions generated by computer simulations.
6. To evaluate alternative refuge deployment strategies for TC1507 maize, such as seed mixes or refuge-in-a-bag. In designing functional refuge deployment strategies, some of the aspects that one must take into account include the biology of the insect pest in question and also aspects specific to insect-plant interactions. For example, there are two FAW strains (rice and maize strains) that are morphologically identical but genetically distinct. These strains also differ physiologically and behaviorally. A better understanding of the biology of these host strains would serve as a tool to more accurately generate predictions of fall armyworm population behavior in the field (Nagoshi and Meagher (2004) *Florida Entomol.* 87:440-449). Another behavioral component that is important in designing refuge deployment strategies is insect dispersal both in larval and adult stages. Adult dispersal patterns may have an impact on random mating of susceptible and potential resistance individuals that emerge from transgenic fields, depending on refuge placement (Hunt et al. (2001) *J. Econ. Entomol.* 94:1369-1377). Also, while considering seed mix as a refuge strategy, one must take into account whether differential survival of heterozygous insects would be favored in case of larval movement between plants (Davis and Onstad (2000) *J. Econ. Entomol.* 93:937-948).
 7. To investigate whether or not existing fall armyworm control tactics, namely MON810, Bt11, MIR162, and chemical insecticides, will affect the rate at which fall armyworm may develop resistance to TC1507 under natural field conditions. This information would be generated based on the presence or absence of cross-resistance between or across insect control tactics used in the geographic locations in question.
 8. To develop molecular marker technology to monitor for development of resistance (change in resistant alleles' frequency) in field populations. This can be done by estimating frequency of resistance alleles in populations where resistance has not evolved using either an F1 or F2 screen, as described by Gould et al. ((1997) *PNAS* 94:3519-3523) and Andow and Alstad ((1998) *J. Econ. Entomol.* 91:572-578), respectively.
 9. To provide a better understanding on the mode of action of Cry1F toxin in the control of FAW. It is generally accepted that steps involved in Bt mode of action include toxin solubilization, enzymatic activation, and binding to midgut receptors (Knowles (1994) *Advances Insect Physiol.* 24:275-308; Schnepf et al. (1998) *Microbiol. Mol. Biol. Rev.* 62:775-806; Bravo et al. (2007) *Toxicon* 49:423-435). Each of the several steps involved in Bt mode of action represent an opportunity for insect adaptation that could result in reduced susceptibility or even complete resistance to Bt exposure (Schnepf et al. (1998) *Microbiol. Mol. Biol. Rev.* 62:775-806; Ferré and J. Van Rie (2002) *Annu. Rev. Entomol.* 47:501-533; Bravo and Soberón (2008) *Trends Biotechnol.* 26:573-579). Reduced susceptibility also could manifest itself in the form of gut regeneration, toxin sequestration or behavioral modification (Lockwood et al. (1984) *Bull. Entomological Soc. America* 30:41-51; Heckel et al. (2007) *J. Invertebrate Pathol.* 95:192-197). Nevertheless, receptor alterations are the most frequently

reported form of Bt resistance (Ferré and J. Van Rie (2002) *Annu. Rev. Entomol.* 47:501-533). Bt mode of action is complex and pathways of toxicity cannot be defined by any single technique. Clearly differentiating the mode of action of one toxin from another can require a combination of approaches such as structural analyses, receptor binding studies (Hua et al. (2001) *Appl. Environ. Microbiol.* 67:872-879; Sena et al. (2009) *Appl. Environ. Microbiol.* 75:2236-2237), pore formation studies (Chen et al. (1993) *PNAS* 90:9041-9045; Lee et al. (2003) *Appl. Environ. Entomol.* 69:4648-4657), and cross-resistance assessments (Pereira et al. (2008) *Entomologia Experimentalis et Applicata* 126:115-121; Hernández-Martínez et al. (2009) *Pest Manag. Sci.* 65:645-650).

It is recognized that methods of using a field-derived colony of FAW disclosed herein above and below can be used with other insect pests of interest that have evolved resistance in the field to one or more insecticidal toxins that are expressed in at least one plant, particular crop plants, more particularly transgenic crop plants that express an insecticidal toxin such as, for example, a Bt toxin.

Insect pests of interest of the present invention include, but are not limited to, insects selected from the orders Coleoptera, Diptera, Hymenoptera, Lepidoptera, Mallophaga, Homoptera, Hemiptera, Orthoptera, Thysanoptera, Dermaptera, Isoptera, Anoplura, Siphonaptera, Trichoptera, etc., particularly Coleoptera and Lepidoptera.

Insects of the order Lepidoptera include, but are not limited to, armyworms, cutworms, loopers, and heliothines in the family Noctuidae *Agrotis ipsilon* Hufnagel (black cutworm); *A. orthogonia* Morrison (western cutworm); *A. segetum* Denis & Schiffermüller (turnip moth); *A. subterranea* Fabricius (granulate cutworm); *Alabama argillacea* Hübner (cotton leaf worm); *Anticarsia gemmatilis* Hübner (velvetbean caterpillar); *Athetis mindara* Barnes and McDunnough (rough skinned cutworm); *Earias insulana* Boisduval (spiny bollworm); *E. vittella* Fabricius (spotted bollworm); *Egira (Xylomyges) curialis* Grote (citrus cutworm); *Euxoa messoria* Harris (dark-sided cutworm); *Helicoverpa armigera* Hübner (American bollworm); *H. zea* Boddie (corn earworm or cotton bollworm); *Heliothis virescens* Fabricius (tobacco budworm); *Hypena scabra* Fabricius (green cloverworm); *Hyponeuma taltula* Schaus; (*Mamestra configurata* Walker (bertha armyworm); *M. brassicae* Linnaeus (cabbage moth); *Melanchra picta* Harris (zebra caterpillar); *Mocis latipes* Guenée (small mocis moth); *Pseudaletia unipuncta* Haworth (armyworm); *Pseudoplusia includens* Walker (soybean looper); *Richia albicosta* Smith (Western bean cutworm); *Spodoptera frugiperda* J E Smith (fall armyworm); *S. exigua* Hubner (beet armyworm); *S. litura* Fabricius (tobacco cutworm, cluster caterpillar); *Trichoplusia ni* Hubner (cabbage looper); borers, casebearers, webworms, coneworms, and skeletonizers from the families Pyralidae and Crambidae such as *Achroia grisella* Fabricius (lesser wax moth); *Amyelois transitella* Walker (naval orangeworm); *Anagasta kuehniella* Zeller (Mediterranean flour moth); *Cadra cautella* Walker (almond moth); *Chilo partellus* Swinhoe (spotted stalk borer); *C. suppressalis* Walker (striped stem/rice borer); *C. terrenellus* Pagenstecher (sugarcane stemp borer); *Corcyra cephalonica* Stainton (rice moth); *Crambus caliginosellus* Clemens (corn root webworm); *C. teterrellus* Zincken (bluegrass webworm); *Cnaphalocrocis medinalis* Guenée (rice leaf roller); *Desmia funeralis* Hübner (grape leaf folder); *Diaphania hyalinata* Linnaeus (melon worm); *D. nitidalis* Stoll (pickleworm); *Diatraea flavipennella* Box; *D. grandiosella* Dyar (southwestern corn borer); *D. saccharalis* Fabri-

cus (sugarcane borer); *Elasmopalpus lignosellus* Zeller (lesser cornstalk borer); *Eoreuma loftini* Dyar (Mexican rice borer); *Ephestia elutella* Hübner (tobacco (cacao) moth); *Galleria mellonella* Linnaeus (greater wax moth); *Hedylepta accepta* Butler (sugarcane leafroller); *Herpetogramma licarsisalis* Walker (sod webworm); *Homoeosoma electellum* Hulst (sunflower moth); *Loxostege sticticalis* Linnaeus (beet webworm); *Maruca testulalis* Geyer (bean pod borer); *Orthaga thyrsalis* Walker (tea tree web moth); *Ostrinia nubilalis* Hübner (European corn borer); *Plodia interpunctella* Hübner (Indian meal moth); *Scirpophaga incertulas* Walker (yellow stem borer); *Udea rubigalis* Guenée (celery leaf tier); and leafrollers, budworms, seed worms, and fruit worms in the family Tortricidae *Acleris gloverana* Walsingham (Western blackheaded budworm); *A. variana* Fernald (Eastern blackheaded budworm); *Adoxophyes orana* Fischer von Rösslerstamm (summer fruit tortrix moth); *Archips* spp. including *A. argyrospila* Walker (fruit tree leaf roller) and *A. rosana* Linnaeus (European leaf roller); *Argyrotaenia* spp.; *Bonagota salubricola* Meyrick (Brazilian apple leafroller); *Choristoneura* spp.; *Cochylis hospes* Walsingham (banded sunflower moth); *Cydia latiferreana* Walsingham (filbert worm); *C. pomonella* Linnaeus (codling moth); *Endopiza viteana* Clemens (grape berry moth); *Eupoecilia ambiguella* Hübner (vine moth); *Grapholita molesta* Busck (oriental fruit moth); *Lobesia botrana* Denis & Schiffermüller (European grape vine moth); *Platynota flavedana* Clemens (variegated leafroller); *P. stultana* Walsingham (omnivorous leafroller); *Spilonota ocellana* Denis & Schiffermüller (eyespot bud moth); and *Suleima helianthana* Riley (sunflower bud moth).

Selected other agronomic pests in the order Lepidoptera include, but are not limited to, *Alsophila pometaria* Harris (fall cankerworm); *Anarsia lineatella* Zeller (peach twig borer); *Anisota senatoria* J. E. Smith (orange striped oak worm); *Antheraea pernyi* Guérin-Ménéville (Chinese Oak Silkmoth); *Bombyx mori* Linnaeus (Silkworm); *Bucculatrix thurberiella* Busck (cotton leaf perforator); *Colias eurytheme* Boisduval (alfalfa caterpillar); *Datana integerrima* Grote & Robinson (walnut caterpillar); *Dendrolimus sibiricus* Tschetwerikov (Siberian silk moth); *Ennomos subsignaria* Hübner (elm spanworm); *Erannis tiliaria* Harris (linden looper); *Erechthias flavistriata* Walsingham (sugarcane bud moth); *Euproctis chrysorrhoea* Linnaeus (browntail moth); *Harrisina americana* Guérin-Ménéville (grapeleaf skeletonizer); *Heliothis subflexa* Guenée; *Hemileuca oliviae* Cockrell (range caterpillar); *Hyphantria cunea* Drury (fall webworm); *Keiferia lycopersicella* Walsingham (tomato pinworm); *Lambdina fiscellaria fiscellaria* Hulst (Eastern hemlock looper); *L. fiscellaria lugubrosa* Hulst (Western hemlock looper); *Leucoma salicis* Linnaeus (satin moth); *Lymantria dispar* Linnaeus (gypsy moth); *Malacosoma* spp.; *Manduca quinquemaculata* Haworth (five spotted hawk moth, tomato hornworm); *M. sexta* Haworth (tomato hornworm, tobacco hornworm); *Operophtera brumata* Linnaeus (winter moth); *Orgyia* spp.; *Paleacrita vernata* Peck (spring cankerworm); *Papilio cresphontes* Cramer (giant swallowtail, orange dog); *Phryganidia californica* Packard (California oakworm); *Phyllocnistis citrella* Stainton (citrus leafminer); *Phyllonorycter blancardella* Fabricius (spotted tentiform leafminer); *Pieris brassicae* Linnaeus (large white butterfly); *P. rapae* Linnaeus (small white butterfly); *P. napi* Linnaeus (green veined white butterfly); *Platyptilia carduidactyla* Riley (artichoke plume moth); *Plutella xylostella* Linnaeus (diamond-back moth); *Pectinophora gossypiella* Saunders (pink bollworm); *Pontia protodice* Boisduval & Leconte (Southern cabbage worm); *Sabulodes aegrotata* Guenée (omnivorous looper); *Schizura concinna* J. E. Smith (red humped caterpil-

lar); *Sitotroga cerealella* Olivier (Angoumois grain moth); *Telechin licus* Drury (giant sugarcane borer); *Thaumetopoea pityocampa* Schiffenmüller (pine processionary caterpillar); *Tineola bisselliella* Hummel (webbing clothesmoth); *Tuta absoluta* Meyrick (tomato leafminer) and *Yponomeuta padella* Linnaeus (ermine moth).

Of interest are larvae and adults of the order Coleoptera including weevils from the families Anthribidae, Bruchidae, and Curculionidae including, but not limited to: *Anthonomus grandis* Boheman (boll weevil); *Cylindrocopturus adspersus* LeConte (sunflower stem weevil); *Diaprepes abbreviatus* Linnaeus (Diaprepes root weevil); *Hypera punctata* Fabricius (clover leaf weevil); *Lissorhoptrus oryzophilus* Kuschel (rice water weevil); *Metamasius hemipterus* hemipterus Linnaeus (West Indian cane weevil); *M. hemipterus sericeus* Olivier (silky cane weevil); *Sitophilus granarius* Linnaeus (granary weevil); *S. oryzae* Linnaeus (rice weevil); *Smicronyx fulvus* LeConte (red sunflower seed weevil); *S. sordidus* LeConte (gray sunflower seed weevil); *Sphenophorus maidis* Chittenden (maize billbug); *S. livis* Vaurie (sugarcane weevil); *Rhabdoscelus obscurus* Boisduval (New Guinea sugarcane weevil); flea beetles, cucumber beetles, rootworms, leaf beetles, potato beetles, and leafminers in the family Chrysomelidae including, but not limited to: *Chaetocnema ectypa* Horn (desert corn flea beetle); *C. pulicaria* Melsheimer (corn flea beetle); *Colaspis brunnea* Fabricius (grape colaspis); *Diabrotica barberi* Smith & Lawrence (northern corn rootworm); *D. undecimpunctata howardi* Barber (southern corn rootworm); *D. virgifera virgifera* LeConte (western corn rootworm); *Leptinotarsa decemlineata* Say (Colorado potato beetle); *Oulema melanopus* Linnaeus (cereal leaf beetle); *Phyllotreta cruciferae* Goeze (corn flea beetle); *Zygogramma exclamationis* Fabricius (sunflower beetle); beetles from the family Coccinellidae including, but not limited to: *Epilachna varivestis* Mulsant (Mexican bean beetle); chafers and other beetles from the family Scarabaeidae including, but not limited to: *Antitrogon parvulus* Britton (Childers cane grub); *Cyclocephala borealis* Arrow (northern masked chafer, white grub); *C. immaculata* Olivier (southern masked chafer, white grub); *Dermolepida albobirtum* Waterhouse (Greyback cane beetle); *Euethola humilis rugiceps* LeConte (sugarcane beetle); *Lepidiota frenchi* Blackburn (French's cane grub); *Tomarus gibbosus* De Geer (carrot beetle); *T. subtropicus* Blatchley (sugarcane grub); *Phyllophaga crinita* Burmeister (white grub); *P. latifrons* LeConte (June beetle); *Popillia japonica* Newman (Japanese beetle); *Rhizotrogus majalis* Razoumowsky (European chafer); carpet beetles from the family Dermestidae; wireworms from the family Elateridae, *Eleodes* spp., *Melanotus* spp. including *M. communis* Gyllenhal (wireworm); *Conoderus* spp.; *Limonius* spp.; *Agriotes* spp.; *Ctenicera* spp.; *Aeolus* spp.; bark beetles from the family Scolytidae; beetles from the family Tenebrionidae; beetles from the family Cerambycidae such as, but not limited to, *Migdolus fryanus* Westwood (longhorn beetle); and beetles from the Buprestidae family including, but not limited to, *Aphanisticus cochinchinae seminulum* Obenberger (leaf-mining buprestid beetle).

Adults and immatures of the order Diptera are of interest, including leafminers *Agromyza parvicornis* Loew (corn blotch leafminer); midges including, but not limited to: *Contarinia sorghicola* Coquillett (sorghum midge); *Mayetiola destructor* Say (Hessian fly); *Neolasioptera murtfeldtiana* Felt, (sunflower seed midge); *Sitodiplosis mosellana* Géhin (wheat midge); fruit flies (Tephritidae), *Oscinella frit* Linnaeus (frit flies); maggots including, but not limited to: *Delia* spp. including *Delia platura* Meigen (seedcorn maggot); *D. coarctata* Fallen (wheat bulb fly); *Fannia canicularis* Lin-

naeus, *F. femoralis* Stein (lesser house flies); *Meromyza americana* Fitch (wheat stem maggot); *Musca domestica* Linnaeus (house flies); *Stomoxys calcitrans* Linnaeus (stable flies); face flies, horn flies, blow flies, *Chrysomya* spp.; *Phormia* spp.; and other muscoid fly pests, horse flies *Tabanus* spp.; bot flies *Gastrophilus* spp.; *Oestrus* spp.; cattle grubs *Hypoderma* spp.; deer flies *Chrysops* spp.; *Melophagus ovinus* Linnaeus (keds); and other Brachycera, mosquitoes *Aedes* spp.; *Anopheles* spp.; *Culex* spp.; black flies *Prosimulium* spp.; *Simulium* spp.; biting midges, sand flies, sciarids, and other Nematocera.

Included as insects of interest are those of the order Hemiptera such as, but not limited to, the following families: Adelgidae, Aleyrodidae, Aphididae, Asterolecaniidae, Cercopidae, Cicadellidae, Cicadidae, Cixiidae, Coccidae, Coreidae, Dactylopiidae, Delphacidae, Diaspididae, Eriococcidae, Flatidae, Fulgoridae, Issidae, Lygaeidae, Margarodidae, Membracidae, Miridae, Ortheziidae, Pentatomidae, Phoenicococcidae, Phylloxeridae, Pseudococcidae, Psyllidae, Pyrrhocoridae and Tingidae.

Agronomically important members from the order Hemiptera include, but are not limited to: *Acrosternum hilare* Say (green stink bug); *Acyrtosiphon pisum* Harris (pea aphid); *Adelges* spp. (adelgids); *Adelphocoris rapidus* Say (rapid plant bug); *Anasa tristis* De Geer (squash bug); *Aphis craccivora* Koch (cowpea aphid); *A. fabae* Scopoli (black bean aphid); *A. gossypii* Glover (cotton aphid, melon aphid); *A. maidiradicis* Forbes (corn root aphid); *A. pomi* De Geer (apple aphid); *A. spiraeicola* Patch (spirea aphid); *Aulacaspis tegalensis* Zehntner (sugarcane scale); *Aulacorthum solani* Kaltenbach (foxglove aphid); *Bemisia tabaci* Gennadius (tobacco whitefly, sweetpotato whitefly); *B. argentifolii* Bellows & Perring (silverleaf whitefly); *Blissus leucopterus leucopterus* Say (chinch bug); Blotomatidae spp.; *Brevicoryne brassicae* Linnaeus (cabbage aphid); *Cacopsylla pyricola* Foerster (pear psylla); *Calocoris norvegicus* Gmelin (potato capsid bug); *Chaetosiphon fragaefolii* Cockerell (strawberry aphid); Cimicidae spp.; Coreidae spp.; *Corythucha gossypii* Fabricius (cotton lace bug); *Cyrtopeltis modesta* Distant (tomato bug); *C. notatus* Distant (suckfly); *Deois flavopicta* Stål (spittlebug); *Dialeurodes citri* Ashmead (citrus whitefly); *Diaphnocoris chlorionis* Say (honeylocust plant bug); *Diuraphis noxia* Kurdjumov/Mordvilko (Russian wheat aphid); *Duplachionaspis divergens* Green (armored scale); *Dysaphis plantaginea* Paaserini (rosy apple aphid); *Dysdercus suturellus* Herrich-Schäffer (cotton stainer); *Dysmicoccus boninsis* Kuwana (gray sugarcane mealybug); *Empoasca fabae* Harris (potato leafhopper); *Eriosoma lanigerum* Hausmann (woolly apple aphid); *Erythroneoura* spp. (grape leafhoppers); *Eumetopina flavipes* Muir (Island sugarcane planthopper); *Eurygaster* spp.; *Euschistus servus* Say (brown stink bug); *E. variolarius* Palisot de Beauvois (one-spotted stink bug); *Graptostethus* spp. (complex of seed bugs); and *Hyalopterus pruni* Geoffroy (mealy plum aphid); *Icerya purchasi* Maskell (cottony cushion scale); *Labopidicola allii* Knight (onion plant bug); *Laodelphax striatellus* Fallen (smaller brown planthopper); *Leptoglossus corculis* Say (leaf-footed pine seed bug); *Leptodictya tabida* Herrich-Schaeffer (sugarcane lace bug); *Lipaphis erysimi* Kaltenbach (turnip aphid); *Lygocoris pabulinus* Linnaeus (common green capsid); *Lygus lineolaris* Palisot de Beauvois (tarnished plant bug); *L. hesperus* Knight (Western tarnished plant bug); *L. pratensis* Linnaeus (common meadow bug); *L. rugulipennis* Poppius (European tarnished plant bug); *Macrosiphum euphorbiae* Thomas (potato aphid); *Macrosteles quadrilineatus* Forbes (aster leafhopper); *Magicicada septendecim* Linnaeus (periodical cicada); *Mahanarva fimbriolata* Stål

(sugarcane spittlebug); *M. posticata* Stål (little cicada of sugarcane); *Melanaphis sacchari* Zehntner (sugarcane aphid); *Melanaspis glomerata* Green (black scale); *Metopolophium dirhodum* Walker (rose grain aphid); *Myzus persicae* Sulzer (peach-potato aphid, green peach aphid); *Nasonovia ribisnigri* Mosley (lettuce aphid); *Nephotettix cincticeps* Uhler (green leafhopper); *N. nigropictus* Stål (rice leafhopper); *Nezara viridula* Linnaeus (southern green stink bug); *Nilaparvata lugens* Stål (brown planthopper); *Nysius ericae* Schilling (false chinch bug); *Nysius raphanus* Howard (false chinch bug); *Oebalus pugnax* Fabricius (rice stink bug); *Oncopeltus fasciatus* Dallas (large milkweed bug); *Orthops campestris* Linnaeus; *Pemphigus* spp. (root aphids and gall aphids); *Peregrinus maidis* Ashmead (corn planthopper); *Perkinsiella saccharicida* Kirkaldy (sugarcane delphacid); *Phylloxera devastatrix* Pergande (pecan phylloxera); *Planococcus citri* Risso (citrus mealybug); *Plesiocoris rugicollis* Fallen (apple capsid); *Poecilopsus lineatus* Fabricius (four-lined plant bug); *Pseudatomoscelis seriatus* Reuter (cotton fleahopper); *Pseudococcus* spp. (other mealybug complex); *Pulvinaria elongata* Newstead (cottony grass scale); *Pyrilla perpusilla* Walker (sugarcane leafhopper); Pyrrhocoridae spp.; *Quadraspidotus perniciosus* Comstock (San Jose scale); Reduviidae spp.; *Rhopalosiphum maidis* Fitch (corn leaf aphid); *R. padi* Linnaeus (bird cherry-oat aphid); *Saccharicoccus sacchari* Cockerell (pink sugarcane mealybug); *Scaptacoris castanea* Perty (brown root stink bug); *Schizaphis graminum* Rondani (greenbug); *Sipha flava* Forbes (yellow sugarcane aphid); *Sitobion avenae* Fabricius (English grain aphid); *Sogatella furcifera* Horvath (white-backed planthopper); *Sogatodes oryzicola* Muir (rice delphacid); *Spanagonicus albofasciatus* Reuter (whitemarked fleahopper); *Therioaphis maculata* Buckton (spotted alfalfa aphid); Tinidae spp.; *Toxoptera aurantii* Boyer de Fonscolombe (black citrus aphid); and *T. citricida* Kirkaldy (brown citrus aphid); *Trialeurodes abutiloneus* (bandedwinged whitefly) and *T. vaporariorum* Westwood (greenhouse whitefly); *Trioza diospyri* Ashmead (persimmon psylla); and *Typhlocyba pomaria* McAtee (white apple leafhopper).

Also included are adults and larvae of the order Acari (mites) such as *Aceria tosichella* Keifer (wheat curl mite); *Panonychus ulmi* Koch (European red mite); *Petrobia latens* Müller (brown wheat mite); *Steneotarsonemus bancrofti* Michael (sugarcane stalk mite); spider mites and red mites in the family Tetranychidae, *Oligonychus grypus* Baker & Pritchard, *O. indicus* Hirst (sugarcane leaf mite), *O. pratensis* Banks (Banks grass mite), *O. stickneyi* McGregor (sugarcane spider mite); *Tetranychus urticae* Koch (two spotted spider mite); *T. mcdanieli* McGregor (McDaniel mite); *T. cinnabarinus* Boisduval (carmine spider mite); *T. turkestanii* Ugarov & Nikolski (strawberry spider mite), flat mites in the family Tenuipalpidae, *Brevipalpus lewisi* McGregor (citrus flat mite); rust and bud mites in the family Eriophyidae and other foliar feeding mites and mites important in human and animal health, i.e. dust mites in the family Epidermoptidae, follicle mites in the family Demodicidae, grain mites in the family Glycyphagidae, ticks in the order Ixodidae, *Ixodes scapularis* Say (deer tick); *I. holocyclus* Neumann (Australian paralysis tick); *Dermacentor variabilis* Say (American dog tick); *Amblyomma americanum* Linnaeus (lone star tick); and scab and itch mites in the families Psoroptidae, Pyemotidae, and Sarcoptidae.

Insect pests of the order Thysanura are of interest, such as *Lepisma saccharina* Linnaeus (silverfish); *Thermobia domestica* Packard (firebrat).

Additional arthropod pests covered include: spiders in the order Araneae such as *Loxosceles reclusa* Gertsch & Mulaik

(brown recluse spider); and the *Latrodectus mactans* Fabricius (black widow spider); and centipedes in the order Scutigermorpha such as *Scutigera coleoptrata* Linnaeus (house centipede). In addition, insect pests of the order Isoptera are of interest, including those of the termitidae family, such as, but not limited to, *Cornitermes cumulans* Kollar, *Cylindrotermes nordenskiöldi* Holmgren and *Pseudacanthotermes militaris* Hagen (sugarcane termite); as well as those in the Rhinotermitidae family including, but not limited to *Heterotermes tenuis* Hagen. Insects of the order Thysanoptera are also of interest, including but not limited to thrips, such as *Stenchaetothrips minutus* van Deventer (sugarcane thrips).

The present invention with any plant species that expresses an insecticidal toxin, particularly transgenic plants that have been engineered to express an insecticidal toxin, more particularly crop plants that have been engineered to express an insecticidal toxin. Plant species of the invention include, but not limited to, monocots and dicots. Examples of plant species of interest include, but are not limited to, corn (*Zea mays*), *Brassica* sp. (e.g., *B. napus*, *B. rapa*, *B. juncea*), particularly those *Brassica* species useful as sources of seed oil, alfalfa (*Medicago sativa*), rice (*Oryza sativa*), rye (*Secale cereale*), sorghum (*Sorghum bicolor*, *Sorghum vulgare*), millet (e.g., pearl millet (*Pennisetum glaucum*), proso millet (*Panicum miliaceum*), foxtail millet (*Setaria italica*), finger millet (*Eleusine coracana*)), sunflower (*Helianthus annuus*), safflower (*Carthamus tinctorius*), wheat (*Triticum aestivum*), soybean (*Glycine max*), tobacco (*Nicotiana tabacum*), potato (*Solanum tuberosum*), peanuts (*Arachis hypogaea*), cotton (*Gossypium barbadense*, *Gossypium hirsutum*), sweet potato (*Ipomoea batatas*), cassava (*Manihot esculenta*), coffee (*Coffea* spp.), coconut (*Cocos nucifera*), pineapple (*Ananas comosus*), citrus trees (*Citrus* spp.), cocoa (*Theobroma cacao*), tea (*Camellia sinensis*), banana (*Musa* spp.), avocado (*Persea americana*), fig (*Ficus casica*), guava (*Psidium guajava*), mango (*Mangifera indica*), olive (*Olea europaea*), papaya (*Carica papaya*), cashew (*Anacardium occidentale*), macadamia (*Macadamia integrifolia*), almond (*Prunus amygdalus*), sugar beets (*Beta vulgaris*), sugarcane (*Saccharum* spp.), oats, barley, vegetables, ornamentals, and conifers.

Vegetables include tomatoes (*Lycopersicon esculentum*), lettuce (e.g., *Lactuca sativa*), green beans (*Phaseolus vulgaris*), lima beans (*Phaseolus limensis*), peas (*Lathyrus* spp.), and members of the genus *Cucumis* such as cucumber (*C. sativus*), cantaloupe (*C. cantalupensis*), and musk melon (*C. melo*). Ornamentals include azalea (*Rhododendron* spp.), hydrangea (*Macrophylla hydrangea*), hibiscus (*Hibiscus rosasanensis*), roses (*Rosa* spp.), tulips (*Tulipa* spp.), daffodils (*Narcissus* spp.), petunias (*Petunia hybrida*), carnation (*Dianthus caryophyllus*), poinsettia (*Euphorbia pulcherrima*), and chrysanthemum.

Conifers that may be employed in practicing the present invention include, for example, pines such as loblolly pine (*Pinus taeda*), slash pine (*Pinus elliotii*), ponderosa pine (*Pinus ponderosa*), lodgepole pine (*Pinus contorta*), and Monterey pine (*Pinus radiata*); Douglas-fir (*Pseudotsuga menziesii*); Western hemlock (*Tsuga canadensis*); Sitka spruce (*Picea glauca*); redwood (*Sequoia sempervirens*); true firs such as silver fir (*Abies amabilis*) and balsam fir (*Abies balsamea*); and cedars such as Western red cedar (*Thuja plicata*) and Alaska yellow-cedar (*Chamaecyparis nootkatensis*). In specific embodiments, plants of the present invention are crop plants (for example, corn, alfalfa, sunflower, *Brassica*, soybean, cotton, safflower, peanut, sorghum, wheat, millet, tobacco, etc.). In other embodiments, corn and cotton plants are optimal, and in yet other embodiments corn plants are optimal.

The methods of the present invention can be used with any insecticidal toxin that can be expressed in a plant to provide resistance to the plant to one or more insect pests of the invention. In some embodiments, the insecticidal protein is a δ -endotoxin of *Bacillus* spp. or derivatives thereof that comprise insecticidal activity. Such δ -endotoxin and synthetic derivatives are referred to herein as Bt toxins. The specific activity of Bt toxins is considered highly beneficial. Unlike most insecticides, the Bt toxins do not have a broad spectrum of activity, so they typically do not kill beneficial insects. Furthermore, the Bt toxins are non-toxic to mammals, including humans, domesticated animals, and wildlife. In particular embodiments, the Bt toxins is a Cry protein.

A list of some known δ -endotoxins (Cry and Cyt endotoxins) and their GenBank Accession Numbers are listed in Table 1. Any of these insecticidal toxins can be expressed in a plant and used as the insecticidal toxin in methods disclosed herein. Moreover, it is recognized that derivatives of any one or more of these insecticidal proteins can be made using method known in the art such as for example DNA shuffling to produce insecticidal toxins comprising, for example, increased insecticidal activity against a pest of interest and/or to alter the target pest specificity of the insecticidal toxin. The use of such derivatives in the methods disclosed here is encompassed by the present invention.

TABLE 1

Some Known δ -endotoxins and their GenBank ® Accession Nos.	
Endotoxin	GenBank ® Accession No.
Cry1Aa1	AAA22353
Cry1Aa2	AAA22552
Cry1Aa3	BAA00257
Cry1Aa4	CAA31886
Cry1Aa5	BAA04468
Cry1Aa6	AAA86265
Cry1Aa7	AAD46139
Cry1Aa8	I26149
Cry1Aa9	BAA77213
Cry1Aa10	AAD55382
Cry1Aa11	CAA70856
Cry1Aa12	AAP80146
Cry1Aa13	AAM44305
Cry1Aa14	AAP40639
Cry1Aa15	AAV66993
Cry1Ab1	AAA22330
Cry1Ab2	AAA22613
Cry1Ab3	AAA22561
Cry1Ab4	BAA00071
Cry1Ab5	CAA28405
Cry1Ab6	AAA22420
Cry1Ab7	CAA31620
Cry1Ab8	AAA22551
Cry1Ab9	CAA38701
Cry1Ab10	A29125
Cry1Ab11	I12419
Cry1Ab12	AAC64003
Cry1Ab13	AAN76494
Cry1Ab14	AAG16877
Cry1Ab15	AAO13302
Cry1Ab16	AAK55546
Cry1Ab17	AAT46415
Cry1Ab18	AAQ88259
Cry1Ab19	AAW31761
Cry1Ab20	ABB72460
Cry1Ab21	ABS18384
Cry1Ab22	ABW87320
Cry1Ab-like	AAK14336
Cry1Ab-like	AAK14337
Cry1Ab-like	AAK14338
Cry1Ab-like	ABG88858
Cry1Ac1	AAA22331
Cry1Ac2	AAA22338

TABLE 1-continued

Some Known δ -endotoxins and their GenBank ® Accession Nos.	
Endotoxin	GenBank ® Accession No.
Cry1Ac3	CAA38098
Cry1Ac4	AAA73077
Cry1Ac5	AAA22339
Cry1Ac6	AAA86266
Cry1Ac7	AAB46989
Cry1Ac8	AAC44841
Cry1Ac9	AAB49768
Cry1Ac10	CAA05505
Cry1Ac11	CAA10270
Cry1Ac12	I12418
Cry1Ac13	AAD38701
Cry1Ac14	AAQ06607
Cry1Ac15	AAN07788
Cry1Ac16	AAU87037
Cry1Ac17	AAV18704
Cry1Ac18	AAV88347
Cry1Ac19	ABD37053
Cry1Ac20	ABB89046
Cry1Ac21	AAV66992
Cry1Ac22	ABZ01836
Cry1Ac23	CAQ30431
Cry1Ac24	ABL01535
Cry1Ac25	FJ513324
Cry1Ac26	FJ617446
Cry1Ac27	FJ617447
Cry1Ac28	ACM90319
Cry1Ad1	AAA22340
Cry1Ad2	CAA01880
Cry1Ae1	AAA22410
Cry1Af1	AAB82749
Cry1Ag1	AAD46137
Cry1Ah1	AAQ14326
Cry1Ah2	ABB76664
Cry1Ai1	AAO39719
Cry1A-like	AAK14339
Cry1Ba1	CAA29898
Cry1Ba2	CAA65003
Cry1Ba3	AAK63251
Cry1Ba4	AAK51084
Cry1Ba5	ABO20894
Cry1Ba6	ABL60921
Cry1Bb1	AAA22344
Cry1Bc1	CAA86568
Cry1Bd1	AAD10292
Cry1Bd2	AAM93496
Cry1Be1	AAC32850
Cry1Be2	AAQ52387
Cry1Be3	FJ716102
Cry1Bf1	CAC50778
Cry1Bf2	AAQ52380
Cry1Bg1	AAO39720
Cry1Ca1	CAA30396
Cry1Ca2	CAA31951
Cry1Ca3	AAA22343
Cry1Ca4	CAA01886
Cry1Ca5	CAA65457
Cry1Ca6	AAF37224
Cry1Ca7	AAG50438
Cry1Ca8	AAM00264
Cry1Ca9	AAL79362
Cry1Ca10	AAN16462
Cry1Ca11	AAV53094
Cry1Cb1	M97880
Cry1Cb2	AAG35409
Cry1Cb3	ACD50894
Cry1Cb-like	AAV63901
Cry1Da1	CAA38099
Cry1Da2	I76415
Cry1Db1	CAA80234
Cry1Db2	AAK48937
Cry1De1	ABK35074
Cry1Ea1	CAA37933
Cry1Ea2	CAA39609
Cry1Ea3	AAA22345
Cry1Ea4	AAD04732
Cry1Ea5	A15535

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TABLE 1-continued

Some Known δ -endotoxins and their GenBank ® Accession Nos.	
Endotoxin	GenBank ® Accession No.
Cry1Ea6	AAL50330
Cry1Ea7	AAW72936
Cry1Ea8	ABX11258
Cry1Eb1	AAA22346
Cry1Fa1	AAA22348
Cry1Fa2	AAA22347
Cry1Fb1	CAA80235
Cry1Fb2	BAA25298
Cry1Fb3	AAF21767
Cry1Fb4	AAC10641
Cry1Fb5	AAO13295
Cry1Fb6	ACD50892
Cry1Fb7	ACD50893
Cry1Ga1	CAA80233
Cry1Ga2	CAA70506
Cry1Gb1	AAD10291
Cry1Gb2	AAO13756
Cry1Gc	AAQ52381
Cry1Ha1	CAA80236
Cry1Hb1	AAA79694
Cry1H-like	AAF01213
Cry1Ia1	CAA44633
Cry1Ia2	AAA22354
Cry1Ia3	AAC36999
Cry1Ia4	AAB00958
Cry1Ia5	CAA70124
Cry1Ia6	AAC26910
Cry1Ia7	AAM73516
Cry1Ia8	AAK66742
Cry1Ia9	AAQ08616
Cry1Ia10	AAP86782
Cry1Ia11	CAC85964
Cry1Ia12	AAV53390
Cry1Ia13	ABF83202
Cry1Ia14	ACG63871
Cry1Ia15	FJ617445
Cry1Ia16	FJ617448
Cry1Ib1	AAA82114
Cry1Ib2	ABW88019
Cry1Ib3	ACD75515
Cry1Ic1	AAC62933
Cry1Ic2	AAE71691
Cry1Id1	AAD44366
Cry1Ie1	AAG43526
Cry1If1	AAQ52382
Cry1I-like	AAC31094
Cry1I-like	ABG88859
Cry1Ja1	AAA22341
Cry1Jb1	AAA98959
Cry1Jc1	AAC31092
Cry1Jc2	AAQ52372
Cry1Jd1	CAC50779
Cry1Ka1	AAB00376
Cry1La1	AAS60191
Cry1-like	AAC31091
Cry2Aa1	AAA22335
Cry2Aa2	AAA83516
Cry2Aa3	D86064
Cry2Aa4	AAC04867
Cry2Aa5	CAA10671
Cry2Aa6	CAA10672
Cry2Aa7	CAA10670
Cry2Aa8	AAO13734
Cry2Aa9	AAO13750
Cry2Aa10	AAQ04263
Cry2Aa11	AAQ52384
Cry2Aa12	ABI83671
Cry2Aa13	ABL01536
Cry2Aa14	ACF04939
Cry2Ab1	AAA22342
Cry2Ab2	CAA39075
Cry2Ab3	AAG36762
Cry2Ab4	AAO13296
Cry2Ab5	AAQ04609
Cry2Ab6	AAP59457
Cry2Ab7	AAZ66347

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TABLE 1-continued

Some Known δ -endotoxins and their GenBank ® Accession Nos.	
Endotoxin	GenBank ® Accession No.
Cry2Ab8	ABC95996
Cry2Ab9	ABC74968
Cry2Ab10	EF157306
Cry2Ab11	CAM84575
Cry2Ab12	ABM21764
Cry2Ab13	ACG76120
Cry2Ab14	ACG76121
Cry2Ac1	CAA40536
Cry2Ac2	AAG35410
Cry2Ac3	AAQ52385
Cry2Ac4	ABC95997
Cry2Ac5	ABC74969
Cry2Ac6	ABC74793
Cry2Ac7	CAL18690
Cry2Ac8	CAM09325
Cry2Ac9	CAM09326
Cry2Ac10	ABN15104
Cry2Ac11	CAM83895
Cry2Ac12	CAM83896
Cry2Ad1	AAF09583
Cry2Ad2	ABC86927
Cry2Ad3	CAK29504
Cry2Ad4	CAM32331
Cry2Ad5	CAO78739
Cry2Ae1	AAQ52362
Cry2Af1	ABO30519
Cry2Ag	ACH91610
Cry2Ah	EU939453
Cry2Ah2	ACL80665
Cry2Ai	FJ788388
Cry3Aa1	AAA22336
Cry3Aa2	AAA22541
Cry3Aa3	CAA68482
Cry3Aa4	AAA22542
Cry3Aa5	AAA50255
Cry3Aa6	AAC43266
Cry3Aa7	CAB41411
Cry3Aa8	AAS79487
Cry3Aa9	AAW05659
Cry3Aa10	AAU29411
Cry3Aa11	AAW82872
Cry3Aa12	ABY49136
Cry3Ba1	CAA34983
Cry3Ba2	CAA00645
Cry3Bb1	AAA22334
Cry3Bb2	AAA74198
Cry3Bb3	I15475
Cry3Ca1	CAA42469
Cry4Aa1	CAA68485
Cry4Aa2	BAA00179
Cry4Aa3	CAD30148
Cry4A-like	AAV96321
Cry4Ba1	CAA30312
Cry4Ba2	CAA30114
Cry4Ba3	AAA22337
Cry4Ba4	BAA00178
Cry4Ba5	CAD30095
Cry4Ba-like	ABC47686
Cry4Ca1	EU646202
Cry4Cb1	FJ403208
Cry4Cb2	FJ597622
Cry4Cc1	FJ403207
Cry5Aa1	AAA67694
Cry5Ab1	AAA67693
Cry5Ac1	I34543
Cry5Ad1	ABQ82087
Cry5Ba1	AAA68598
Cry5Ba2	ABW88932
Cry6Aa1	AAA22357
Cry6Aa2	AAM46849
Cry6Aa3	ABH03377
Cry6Ba1	AAA22358
Cry7Aa1	AAA22351
Cry7Ab1	AAA21120
Cry7Ab2	AAA21121
Cry7Ab3	ABX24522

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TABLE 1-continued

Some Known δ -endotoxins and their GenBank ® Accession Nos.	
Endotoxin	GenBank ® Accession No.
Cry7Ab4	EU380678
Cry7Ab5	ABX79555
Cry7Ab6	ACI44005
Cry7Ab7	FJ940776
Cry7Ab8	GU145299
Cry7Ba1	ABB70817
Cry7Ca1	ABR67863
Cry7Da1	ACQ99547
Cry8Aa1	AAA21117
Cry8Ab1	EU044830
Cry8Ba1	AAA21118
Cry8Bb1	CAD57542
Cry8Bc1	CAD57543
Cry8Ca1	AAA21119
Cry8Ca2	AAR98783
Cry8Ca3	EU625349
Cry8Da1	BAC07226
Cry8Da2	BD133574
Cry8Da3	BD133575
Cry8Db1	BAF93483
Cry8Ea1	AAQ73470
Cry8Ea2	EU047597
Cry8Fa1	AAT48690
Cry8Ga1	AAT46073
Cry8Ga2	ABC42043
Cry8Ga3	FJ198072
Cry8Ha1	EF465532
Cry8Ja1	EU381044
Cry8Ja1	EU625348
Cry8Ka1	FJ422558
Cry8Ka2	ACN87262
Cry8-like	FJ770571
Cry8-like	ABS53003
Cry9Aa1	CAA41122
Cry9Aa2	CAA41425
Cry9Aa3	GQ249293
Cry9Aa4	GQ249294
Cry9Aa like	AAQ52376
Cry9Ba1	CAA52927
Cry9Bb1	AAV28716
Cry9Ca1	CAA85764
Cry9Ca2	AAQ52375
Cry9Da1	BAA19948
Cry9Da2	AAB97923
Cry9Da3	GQ249295
Cry9Da4	GQ249297
Cry9Db1	AAAX78439
Cry9Ea1	BAA34908
Cry9Ea2	AAO12908
Cry9Ea3	ABM21765
Cry9Ea4	ACE88267
Cry9Ea5	ACF04743
Cry9Ea6	ACG63872
Cry9Ea7	FJ380927
Cry9Ea8	GQ249292
Cry9Eb1	CAC50780
Cry9Eb2	GQ249298
Cry9Ec1	AAC63366
Cry9Ed1	AAAX78440
Cry9Ee1	GQ249296
Cry9-like	AAC63366
Cry10Aa1	AAA22614
Cry10Aa2	E00614
Cry10Aa3	CAD30098
Cry10A-like	DQ167578
Cry11Aa1	AAA22352
Cry11Aa2	AAA22611
Cry11Aa3	CAD30081
Cry11Aa-like	DQ166531
Cry11Ba1	CAA60504
Cry11Bb1	AAC97162
Cry12Aa1	AAA22355
Cry13Aa1	AAA22356
Cry14Aa1	AAA21516
Cry15Aa1	AAA22333
Cry16Aa1	CAA63860

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TABLE 1-continued

Some Known δ -endotoxins and their GenBank ® Accession Nos.	
Endotoxin	GenBank ® Accession No.
Cry17Aa1	CAA67841
Cry18Aa1	CAA67506
Cry18Ba1	AAF89667
Cry18Ca1	AAF89668
Cry19Aa1	CAA68875
Cry19Ba1	BAA32397
Cry20Aa1	AAB93476
Cry20Ba1	ACS93601
Cry20-like	GQ144333
Cry21Aa1	I32932
Cry21Aa2	I66477
Cry21Ba1	BAC06484
Cry22Aa1	I34547
Cry22Aa2	CAD43579
Cry22Aa3	ACD93211
Cry22Ab1	AAK50456
Cry22Ab2	CAD43577
Cry22Ba1	CAD43578
Cry23Aa1	AAF76375
Cry24Aa1	AAC61891
Cry24Ba1	BAD32657
Cry24Ca1	CAJ43600
Cry25Aa1	AAC61892
Cry26Aa1	AAD25075
Cry27Aa1	BAA82796
Cry28Aa1	AAD24189
Cry28Aa2	AAG00235
Cry29Aa1	CAC80985
Cry30Aa1	CAC80986
Cry30Ba1	BAD00052
Cry30Ca1	BAD67157
Cry30Ca2	ACU24781
Cry30Da1	EF095955
Cry30Db1	BAE80088
Cry30Ea1	ACC95445
Cry30Ea2	FJ499389
Cry30Fa1	ACI22625
Cry30Ga1	ACG60020
Cry31Aa1	BAB11757
Cry31Aa2	AAL87458
Cry31Aa3	BAE79808
Cry31Aa4	BAF32571
Cry31Aa5	BAF32572
Cry31Ab1	BAE79809
Cry31Ab2	BAF32570
Cry31Ac1	BAF34368
Cry32Aa1	AAG36711
Cry32Ba1	BAB78601
Cry32Ca1	BAB78602
Cry32Da1	BAB78603
Cry33Aa1	AAL26871
Cry34Aa1	AAG50341
Cry34Aa2	AAK64560
Cry34Aa3	AAT29032
Cry34Aa4	AAT29030
Cry34Ab1	AAG41671
Cry34Ac1	AAG50118
Cry34Ac2	AAK64562
Cry34Ac3	AAT29029
Cry34Ba1	AAK64565
Cry34Ba2	AAT29033
Cry34Ba3	AAT29031
Cry35Aa1	AAG50342
Cry35Aa2	AAK64561
Cry35Aa3	AAT29028
Cry35Aa4	AAT29025
Cry35Ab1	AAG41672
Cry35Ab2	AAK64563
Cry35Ab3	AY536891
Cry35Ac1	AAG50117
Cry35Ba1	AAK64566
Cry35Ba2	AAT29027
Cry35Ba3	AAT29026
Cry36Aa1	AAK64558
Cry37Aa1	AAF76376
Cry38Aa1	AAK64559

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TABLE 1-continued

Some Known δ -endotoxins and their GenBank ® Accession Nos.	
Endotoxin	GenBank ® Accession No.
Cry39Aa1	BAB72016
Cry40Aa1	BAB72018
Cry40Ba1	BAC77648
Cry40Ca1	EU381045
Cry40Da1	ACF15199
Cry41Aa1	BAD35157
Cry41Ab1	BAD35163
Cry42Aa1	BAD35166
Cry43Aa1	BAD15301
Cry43Aa2	BAD95474
Cry43Ba1	BAD15303
Cry43-like	BAD15305
Cry44Aa	BAD08532
Cry45Aa	BAD22577
Cry46Aa	BAC79010
Cry46Aa2	BAG68906
Cry46Ab	BAD35170
Cry47Aa	AAV24695
Cry48Aa	CAJ18351
Cry48Aa2	CAJ86545
Cry48Aa3	CAJ86546
Cry48Ab	CAJ86548
Cry48Ab2	CAJ86549
Cry49Aa	CAH56541
Cry49Aa2	CAJ86541
Cry49Aa3	CAJ86543
Cry49Aa4	CAJ86544
Cry49Ab1	CAJ86542
Cry50Aa1	BAE86999
Cry51Aa1	ABI14444
Cry52Aa1	EF613489
Cry52Ba1	FJ361760
Cry53Aa1	EF633476
Cry53Ab1	FJ361759
Cry54Aa1	ACA52194
Cry55Aa1	ABW88931
Cry55Aa2	AAE33526
Cry56Aa1	FJ597621
Cry56Aa2	GQ483512
Cry57Aa1	ANC87261
Cry58Aa1	ANC87260
Cry59Aa1	ACR43758
Cyt1Aa1	X03182
Cyt1Aa2	X04338
Cyt1Aa3	Y00135
Cyt1Aa4	M35968
Cyt1Aa5	AL731825
Cyt1Aa6	ABC17640
Cyt1Aa-like	ABB01172
Cyt1Ab1	X98793
Cyt1Ba1	U37196
Cyt1Ca1	AL731825
Cyt2Aa1	Z14147
Cyt2Aa2	AF472606
Cyt2Aa3	EU835185
Cyt2Ba1	U52043
Cyt2Ba2	AF020789
Cyt2Ba3	AF022884
Cyt2Ba4	AF022885
Cyt2Ba5	AF022886
Cyt2Ba6	AF034926
Cyt2Ba7	AF215645
Cyt2Ba8	AF215646
Cyt2Ba9	AL731825
Cyt2Ba10	ACX54358
Cyt2Ba11	ACX54359
Cyt2Ba12	ACX54360
Cyt2Ba-like	ABE99695
Cyt2Bb1	U82519
Cyt2Bc1	CAC80987
Cyt2B-like	DQ341380
Cyt2Ca1	AAK50455
Unknown	AAA22332
Unknown	AAL26870
Unknown	CAA63374
Unknown	BAA13073

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TABLE 1-continued

Some Known δ -endotoxins and their GenBank ® Accession Nos.	
Endotoxin	GenBank ® Accession No.
Unknown	CAA67205
Unknown	CAA67329

The following examples are offered by way of illustration and not by way of limitation.

EXAMPLE 1

Production of Field-Derived Fall Armyworm Colony Selected for Decreased Susceptibility to Maize Plants Expressing the Insecticidal Protein Cry1F

A fall armyworm colony exhibiting field-selected resistance to maize expressing event TC1507 was established in a laboratory. The process by which the colony was produced comprised the following steps.

1. The Selected Puerto Rico Colony (FAW-SPR) was initiated by collecting at least 1000 fall armyworm eggs from fields in Puerto Rico in October 2008 and again in January 2009.

2. Upon arrival at the laboratory, the eggs were incubated at approximate 25° C. until hatching. Hatching occurred within 1 day.

3. The recently hatched larvae (neonates) were exposed to Cry1F expressing leaf disks from maize plants comprising event TC1507 and allowed to grow for 4 days. The concentration of Cry1F in the leaf discs was 12.1±6.2 ng/mg leaf tissue dry weight.

4. Survivors were collected and transferred to a standard fall armyworm diet and allowed to complete development. Survivors from both the October 2008 and January 2009 collections were combined.

5. Individuals completing development are allowed to randomly mate in order to maintain the colony.

6. Every three generations, selection in Cry1F-expressing leaf tissue from maize plants comprising event TC1507 is conducted using a population of at least 500 neonates.

EXAMPLE 2

Characterization of Cry1F Resistance in Fall Armyworm Using a Field-Derived Colony

A study was conducted to characterize the susceptibility of the Puerto Rico Colony to Cry1F using a diagnostic assay. Characterization of the FAW-SPR susceptibility to the Bt Cry1F insecticidal toxin was assessed by measuring the effects of feeding FAW-SPR leaf material from maize plants comprising event TC1507 (express Cry1F) on neonates (larvae <24 h after hatch). The test system targeted the use of neonates which were exposed to one leaf disc, of either the test or control substances, in a multi-arena tray. The leaf discs were the only food source for larvae for the duration of the experiment. Fresh leaf discs were added as needed to provide a constant source of food. Greenhouse collected leaves were rinsed with tap water. Multi-arena trays were controlled for humidity by placing a bottom-layer of agar into each well. This test system has already been validated and used for measuring insecticidal effects of plant-incorporated proteins.

Larval exposure to fresh leaf tissue was chosen as a means of administration because it is representative of insect exposure to plant-incorporated protectants in field conditions.

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Moreover, the effects of these insecticidal proteins are both antibiotic and antixenotic, and exposure to plant tissue may be more ecologically realistic. This method of administration was chosen over a diet-based dose-response assay using pure protein or lyophilized plant tissue because of confounding effects that could result from trying to mimic field-relevant larval exposure.

The test substance was fresh, greenhouse-grown leaf tissue from hybrid maize plants containing event expressing the *Bacillus thuringiensis* Cry1F insecticidal protein (event TC1507). The control for natural effects of the test system (negative control) was fresh, greenhouse-grown leaf tissue from hybrid maize plants in similar genetic background (isoline maize) containing no events expressing insecticidal proteins (isoline maize). The control had one or both inbred parents in common with the test hybrid.

Tissue from both test and control substances were systematically sampled from similar leaves. Test and control substances were subjected to quantitative ELISA to determine level of Cry1F protein expression in TC1507 tissue and confirm absence of Cry1F protein expression in isoline tissue.

Trays were set up by preparing a 2% agar solution and pipetting 1 ml of warm agar solution into each well of a 128-well tray (CV International). The agar solution was allowed to cool and solidify and a disk of freshly collected corn leaf tissue was placed into each well. As tissue was collected for the experiment leaf punches were obtained for quantitative ELISA and submitted immediately for evaluation. One neonate FAW-SPR was placed in each well and a lid was placed securely to the top of the well to prevent insect escape. Insects were monitored daily for mortality and food reserves. Food was replaced as needed during the duration of the test. Neonate mortality was monitored daily, and mortality counts were taken at the end of the 4 day exposure period.

The trays were placed in a growth chamber with target temperature of 25° C. ($\pm 5^\circ$ C.), relative humidity >60% and total darkness.

The experiment was conducted using a randomized incomplete block design with 32 replicates for test substance and 4 replicates for the control substance. Each replicate consisted of 16 observations per treatment in a multi-arena tray. The experimental unit was composed of an individual well in the 128-well tray (CV International). Each tray was labeled with the study number and individual treatments within each tray were labeled to identify treatment and the replication number using indelible ink. The treatment groups were as follows:

Treatment 1: 512 individuals of FAW-SPR fed leaf material from maize plants comprising the TC1507 event (Cry1F expressing event), and

Treatment 2: 64 individuals of FAW-SPR fed leaf material from isoline maize plants that do not express Cry1F (negative control).

The results of FAW-SPR exposure to leaf material from maize plants expressing event TC1507 are presented in Table 2. No larvae from the susceptible strain (FAW-lab) were able to survive exposure to TC1507 leaf material (Table 2). Data presented shows that the FAW-SPR population was able to survive exposure to TC1507 plant material similarly to its survival on isoline maize plant tissue, suggesting a significantly decreased level of susceptibility to the Cry1F toxin.

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TABLE 2

Response of FAW-SPR and FAW-lab to Feeding on Cry1F-Expressing Leaf Material from TC1507 Maize Plants			
	Plant Material*	No. of Individuals	Mortality (%)
FAW-SPR	TC1507	512	5.2
	Isoline	64	4.7
FAW-lab	TC1507	32	100
	Isoline	32	9.4

*TC1507 plant material comprises Cry1F. Isoline plant material lacks Cry1F.

Thus the present study indicated that the FAW-SPR field collected *S. frugiperda* population exhibited high levels of resistance to Cry1F as shown by the survival of neonates on TC1507 leaf tissue.

The development of a colony of fall armyworm which exhibit such a high degree of resistance presents several opportunities for investigation and use of colonies tolerant to the event. Additionally, because the resistance to the Cry1F was developed in the field, one would expect the FAW-SPR colony to more closely reflect tolerance which naturally develops through repeated field exposure rather than the artificial tolerance developed through progressive exposure in the lab.

EXAMPLE 3

Further Characterization of Cry1F Resistance in Fall Armyworm Using a Field-Derived Colony

The Cry1F resistance that has been identified in fall armyworm (FAW) populations collected from Puerto Rico and used to produce the field-derived colony (FAW-SPR) that is described in Examples 1 and 2 was further characterized and used to estimate the risk of resistance evolution in populations of FAW that are currently susceptible to Cry1F.

1. Develop Genetic Stocks of Resistant FAW and Establish Bioassay Methods to Quantify Resistance Levels

A key step in developing a rational resistance management strategy is to develop laboratory-selected colonies that exhibit high levels of resistance to a particular toxin.

The availability of resistant strains will allow subsequent genetic analysis of resistance inheritance, determination of the biochemical and physiological basis of resistance, and potentially, the development of molecular probes to monitor the evolution of resistance in the field. The resistant colony of FAW from Puerto Rico that is described in Example 1 above will be used as the starting material for the development of the laboratory-selected colonies.

Maintenance of the Cry1F resistant colony will be achieved by exposing neonate larvae to leaf material from maize plants expressing Cry1F. Individual neonate larvae (at least 1,000 per generation) will be exposed to leaf disks from maize hybrids comprising event TC1507. Surviving larvae (those that have initiated feeding and have grown beyond 1st instar) will be transferred to untreated diet and reared to adults using standard rearing techniques.

Bioassay of neonate FAW larvae was conducted to quantify the level of resistance identified in Cry1F resistant strain and to assess cross resistance to other Bt toxins. Bioassays involved techniques previously developed for assays with European corn borer (Marcon et al. 1999). Exposure to Bt toxins were applied to the surface of single wells of artificial diet is performed in 128 well trays (each well 16 mm diameter \times 16 mm height; CD International, Pitman, N.J.). Toxin solutions were prepared in 0.1% Triton-X 100 to obtain uni-

form spreading of Bt solution on the diet surface. Individual neonate larvae were placed in diet-containing wells, and mortality and combined larval weight were recorded seven days later. Control treatments consisted of wells treated with 0.1% Triton-X 100. When recording mortality, larvae that had not grown beyond first instar (i.e., <0.1 mg) were considered to be dead. Bioassays were conducted in duplicate on three different dates and included at least five Bt concentrations that produced mortality >0 but <100%. Data were analyzed by probit analysis (Finney (1971) "Probit analysis," Cambridge University Press, England; LeOra Software (1987) "POLO-PC. A user's guide to probit and logit analysis," Berkeley, Calif.) to determine lethal concentrations. Observed mortality is corrected for mortality in control treatments, and lethal concentrations with 95% fiducial limits are calculated. Larval weights are transformed to % growth inhibition relative to the controls, and these data are analyzed by non-linear regression (Marçon et al. (1999) *J. Econ. Entomol.* 92:2799-285). Bioassays of the selected colony will be compared with at least two unselected laboratory colonies currently available in our laboratory to estimate resistance ratios.

To measure survival of the selected colony on Cry1F expressing corn tissue, leaf discs from V3-V5 corn plants that have been maintained under greenhouse conditions and which have been tested for Cry1F expression using standard immunoassays will be utilized. Leaf discs (0.5 cm diameter) are placed on top of a well of solidified agar in the bioassay trays described above, and a single neonate is placed in each well. Larvae are allowed to feed for four days, and mortality and qualitative estimates of leaf consumption are recorded after four days. Responses to both Cry1F expressing plants and non-Bt isoline plants will be determined for both the selected and control strains.

2. Determine the Inheritance of Resistance (i.e., Dominance, Sex-Linkage, Number of Resistance Genes)

One key component of successful resistance management of any pest species is determination of the genetic expression of resistance (i.e., dominant of recessive, autosomal vs. sex-linked) associated with a given resistance mechanism. Another important factor is to identify the number of genes associated with the resistance. Genetic data are essential to distinguishing between cross-resistance (the occurrence of one mechanism which confers resistance to several different toxins) and multiple resistance (several co-existing mechanisms, each of which confers resistance to one or more different pesticides). Additionally, some resistance management tactics, such as the high-dose/refuge approach proposed for Bt corn, are dependent on a given inheritance pattern although data to support such an inheritance are usually lacking. Finally, the availability of strains of known susceptible and resistant genotypes can be used to improve diagnostic bioassays used in monitoring programs.

The inheritance of Cry1F resistance was determined using reciprocal crosses of resistant and susceptible parents. A portion of the F1 progeny from individual crosses was bioassayed for Bt susceptibility using techniques previously described. The mortality curves were evaluated for sex-linkage and for assessing the degree of dominance (Stone (1968) *Bull. WHO* 38:325-329; Alves et al. (2006) *J. Econ. Entomol.* 99:494-501). Because resistance was due to an autosomal trait, progeny from single pair crosses were back-crossed to either the susceptible or resistant parental strain. The progeny were bioassayed to determine whether the resistance is conferred by a single genetic factor or if multiple genes were involved based on departure from the expected 1:1 ratio of RS to SS genotypes for a single factor inheritance. Response

curves were generated for the various genotypes to estimate allele frequencies (see below).

3. Estimate Frequency of Resistance Alleles in Populations where Resistance has not Evolved Using Either an F1 or F2 Screen to Detect Resistance Alleles

As described by Gould et al. ((1997) *PNAS* 94:3519-3523) if a homozygous resistant strain (RR) is available and resistance is recessive, estimates of resistance allele frequency can be obtained through single pair matings of field collected individuals with resistant individuals from the resistant laboratory colony. Because resistance alleles are most likely to be present in heterozygotes prior to a resistance episode or control failure (Roush and Daly (1990) "The role of population genetics in resistance research and management," In *Pesticide resistance in arthropods*, Roush and Tabashnik, eds., pp. 97-152, Chapman and Hall, NY), single-pair matings of the resistant lab colony (RR) with field collected individuals will result in progeny (F1) that are either 100% RS if the field collected individual is SS or a ratio of 1RR:1RS if the field collected parent carries one resistant allele. Screening these progeny at a concentration of Bt that discriminates between RS and RR genotypes would provide an efficient means of screening for rare resistance alleles. In the absence of a resistant strain, similar estimates of allele frequencies can be determined using an F2 approach (Andow and Alstad (1998) *J. Econ. Entomol.* 91:572-578) in which an inbreeding step allows expression of recessive alleles.

Field collections of FAW were obtained as larvae from corn fields. A non-Bt field was selected that is as far as possible from the nearest Bt field to minimize the possibility that local selection could result in a non-uniform distribution of resistance alleles across the landscape and therefore artificially raise the estimate of resistance allele frequency.

4. Consequences of Resistance on Reproductive Fitness

Trade-offs (negative associations between traits) commonly occur between key organismal traits such as fecundity, longevity, and duration of development and strongly constrain the evolution of individual traits. There is a growing appreciation of the importance in resistance management of identifying trade-offs between resistance and other traits, especially with regard to resistance mitigation. One focus of insect resistance management (IRM) research is to document the existence of trade-offs between resistance and fitness components for resistant strain. The existence of such trade-offs, or lack thereof, will influence the particular strategy used to manage resistance and potentially mitigate a resistance outbreak if it occurs.

Information on the potential trade-offs between resistance to Bt toxin and other organismal features will come from the mechanistic studies of Bt resistance in the resistant field population from Puerto Rico. Before we initiate fitness comparisons, we will establish near isogenic resistant and susceptible lines by repeated crossing and back-crossing combined with selection to minimize genetic differences between strains that might confound assessments of fitness trade-offs. Key fitness traits such as development time, fecundity, and longevity in susceptible and resistant strains will be measures. Pupae will be isolated individually from the resistant and susceptible strains to obtain virgin males and females. Emergent male-female pairs will be held in "honeymoon cages" so that fitness parameters (pupal weight, # egg masses, egg mass weight, time to first oviposition, and longevity) can be recorded for individual pairs (Siegfried et al. (2001) *Entomol. Exper. Appl.* 100: 15-20).

EXAMPLE 4

Level of Resistance in Fall Armyworms from
FAW-SPR

To assess the level of resistance in fall armyworms from FAW-SPR, bioassays were conducted with FAW from the FAW-SPR colony disclosed in Example 1 and susceptible FAW from a laboratory colony. The FAW were exposed to diets comprising varying amounts of Cry1F as described in Example 3. The results of bioassays were used to determine that the susceptible colony had an LC_{50} =18.6 ng/cm², the resistant colony (FAW-SPR) had an LC_{50} of greater than 7200 ng/cm². The diagnostic concentration was also determined to 200 ng/cm² and resistance ratio was greater than or equal to 387.1

EXAMPLE 5

Inheritance of Resistance in Fall Armyworms from
FAW-SPR

To assess the inheritance of resistance in fall armyworms from FAW-SPR, reciprocal crosses between resistant FAW from the FAW-SPR colony disclosed in Example 1 and susceptible FAW were made, the resulting progeny assayed for mortality, and mortality curves prepared as described in Example 3. Backcrosses were also conducted as described in Example 3.

The results of the reciprocal crosses and backcrosses are illustrated in FIGS. 1 and 2, respectively. The results revealed that the inheritance of resistance in FAW-SPR is recessive, autosomal, and conferred by a single gene.

EXAMPLE 6

Frequency of Resistance in Fall Armyworm
Populations in Texas and Florida

Fall Armyworms were collected from fields in Texas and Florida where FAW resistance to Cry1F has not evolved. There is limited interaction between FAW from Puerto Rico where resistance has evolved and FAW in Texas. However, there is known to be a significant exchange between FAW in Puerto Rico and Florida (Nagoshi et al. (2010) *J. Econ. Entomol.* 103:360-367). FAW from FAW-SPR were crossed with individuals from the Texas and Florida populations and the progeny bioassayed for mortality as described in Example 3. The results of the bioassays are summarized in Table 3.

TABLE 3

Frequency of Resistance in Texas and Florida Populations of FAW.		
	Florida	Texas
Families Tested	29	18
#SS	23	18
#Sr	6*	0
#rr	0	0

*Confirmed to be Sr in F₂.

From these results, the frequency of the resistant allele (r) in the Florida population was estimated to be approximately 0.1. In Texas population, the resistance allele was not detected.

The article "a" and "an" are used herein to refer to one or more than one (i.e., to at least one) of the grammatical object of the article. By way of example, "an element" means one or more element.

All publications and patent applications mentioned in the specification are indicative of the level of those skilled in the art to which this invention pertains. All publications, patent applications, and nucleotide and amino sequences referred to by GenBank Accession Numbers are herein incorporated by reference to the same extent as if each individual publication or patent application was specifically and individually indicated to be incorporated by reference.

Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be obvious that certain changes and modifications may be practiced within the scope of the appended claims. Many modifications and other embodiments of the inventions set forth herein will come to mind to one skilled in the art to which these inventions pertain having the benefit of the teachings presented in the foregoing descriptions and the associated drawings. Therefore, it is to be understood that the inventions are not to be limited to the specific embodiments disclosed and that modifications and other embodiments are intended to be included within the scope of the appended claims. Although specific terms are employed herein, they are used in a generic and descriptive sense only and not for purposes of limitation.

That which is claimed:

1. A method for producing a field-derived colony of fall armyworms (FAW) that comprises decreased susceptibility to maize plants producing Cry1F, the method comprising:

- (a) collecting FAW from an agricultural field comprising maize plants that express Cry1F;
 - (b) allowing the FAW to feed on a diet comprising an effective concentration of Cry1F of 200 ng/cm² or greater, wherein the effective concentration is sufficient to kill greater than 50% of the susceptible FAW;
 - (c) selecting the surviving FAW;
 - (d) determining the zygoty of the surviving FAW; and
 - (e) forming a colony of surviving FAW that are homozygous for the field-evolved resistance to Cry1F and has a resistance ratio greater than or equal to 387.
2. The method of claim 1, further comprising:
- (a) mating resistant FAW from the field-derived colony with FAW that are susceptible to Cry1F, whereby progeny are produced; and
 - (b) analyzing the mortality rates of the progeny from each mating when grown in the presence of Cry1F.
3. The method of claim 2, further comprising backcrossing the progeny of (a) with resistant FAW from the field-derived colony.

4. The method of claim 2, wherein analyzing the mortality rates comprises preparing one or mortality curves.

5. The method of claim 2 wherein the method is used for determining the inheritance of resistance of in a field-derived colony of FAW that comprises field-evolved resistance to Cry1F.

6. The method of claim 1, wherein the diet comprises leaf material from maize plants comprising event TC1507.

* * * * *